

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:06:22 ; Search time 48 Seconds
(without alignments)
1336.590 Million cell updates/sec

Title: US-09-874-162a-8
Perfect score: 4078
Sequence: 1 MTGIAAASFNTCRFGCGC.....KALFTDVSQVSKSKQKQL 776

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1127.5	27.6	947	2	US-09-270-767-45347, A Sequence 45347, A
2	987.5	24.2	835	2	US-09-270-767-60845, A Sequence 60845, A
3	661	16.2	243	2	US-10-144-198-16 Sequence 16, Appl
4	661	16.2	243	2	US-10-104-047-2404 Sequence 2404, Ap
5	437.5	10.7	102	2	US-09-513-999C-7263 Sequence 7263, Ap
6	238.5	5.8	604	2	US-09-339-947A-8 Sequence 8, Appl
7	224	5.5	611	2	US-09-339-947A-1 Sequence 1, Appl
8	211	5.2	243	2	US-09-270-767-44285 Sequence 44285, A
9	160	3.9	1401	2	US-08-755-587-186 Sequence 186, App
10	159	3.9	1494	2	US-08-755-587-186 Sequence 186, App
11	156.5	3.8	3696	2	US-09-134-001C-5080 Sequence 5080, Ap
12	153.5	3.8	1279	2	US-09-710-279-3188 Sequence 3188, Ap
13	151.5	3.7	584	2	US-09-248-796A-17551 Sequence 17551, A
14	150	3.7	912	1	US-07-789-915A-8 Sequence 8, Appl
15	150	3.7	912	1	US-08-005-002C-8 Sequence 8, Appl
16	150	3.7	912	1	US-08-487-203A-8 Sequence 8, Appl
17	149	3.7	1087	2	US-09-830-230A-322 Sequence 322, App
18	149	3.7	1119	2	US-09-830-230A-321 Sequence 321, App
19	146.5	3.6	1235	1	US-08-118-101A-2 Sequence 2, Appl
20	142.5	3.5	1972	2	US-09-418-710-21 Sequence 21, Appl
21	142.5	3.5	1972	2	US-09-839-479-21 Sequence 21, Appl
22	139.5	3.4	2446	2	US-09-949-016-11439 Sequence 11439, A
23	137.5	3.4	2954	2	US-09-150-867-1 Sequence 1, Appl
24	135	3.3	3210	2	US-09-538-092-1154 Sequence 1154, Ap
25	135	3.3	3248	1	US-08-353-700-1 Sequence 1, Appl
26	135	3.3	3248	4	PCT-US95-16216-1 Sequence 1, Appl
27	133	3.3	472	2	US-09-248-796A-20611 Sequence 20611, A

28	132	3.2	2482	1	US-08-328-254-6 Sequence 6, Appl
29	131.5	3.2	4377	2	US-09-949-016-6978 Sequence 6978, Ap
30	131	3.2	1147	2	US-09-538-092-1074 Sequence 1074, Ap
31	131	3.2	1602	2	US-09-268-874A-7 Sequence 7, Appl
32	131	3.2	1621	2	US-09-268-874A-5 Sequence 5, Appl
33	131	3.2	1639	2	US-09-268-874A-3 Sequence 3, Appl
34	130.5	3.2	3913	2	US-09-949-016-10933 Sequence 10933, A
35	130	3.2	2375	2	US-09-538-092-1131 Sequence 1131, Ap
36	129.5	3.2	614	2	US-09-248-796A-17642 Sequence 17642, A
37	129	3.2	1164	2	US-09-538-092-399 Sequence 399, App
38	128.5	3.2	907	2	US-08-938-830-26 Sequence 26, Appl
39	128.5	3.2	907	2	US-09-020-222-26 Sequence 26, Appl
40	128.5	3.2	907	2	US-09-068-377-26 Sequence 26, Appl
41	128.5	3.2	1167	2	US-09-803-671B-2 Sequence 2, Appl
42	128.5	3.2	1167	2	US-10-274-409-2 Sequence 2, Appl
43	128.5	3.2	1712	2	US-09-949-016-9450 Sequence 9450, Ap
44	128	3.1	798	2	US-09-203-453-5 Sequence 5, Appl
45	128	3.1	798	2	US-09-900-236-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-270-767-45347
; Sequence 45347, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45347
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45347

Query Match	27.6%	Score 1127.5	DB 2	Length 947
Best Local Similarity	32.9%	Pred. No. 4.7e-96		
Matches	273	Conservative 137	Mismatches 240	Indels 179
Gaps	26			
QY	65	MTDAARBOESLKKKIOPKSLTSSVSNGV---	STPRHSGSLTPVTPPTPSS	120
DB	1	MAPAKKEKOS-----	NPDGSAANGIIIGLTGAPASNAGSTVPPTAGQVTLN	49
QY	121	SFRSTP-----	TEPTQIVRFLRTMLAPRPHRTLTWSHNSRPNRKTKPKYUDM	174
DB	50	GHOEOBELFLQAFKPPQIYKRLNREHNPFIPLNKLSTYKEMSRNKRISFOVNSM		109
QY	175	LSKYEKKMGEOESHLSA-HLQLTFTGFPHKNDKPSNSENQ-----	NSVTLLE	222
DB	110	LEST-----	TQKSAVSAQNTLHVLYDSLHETLPRALDNESGDDLLQOLCEABASVSVE	164
QY	223	VLVYKVCCHKRKVDSCIRQVPTGKKOYPLIPDINQTKPGNPSLAVSNSEFP-SNSHM	281	
DB	165	TTLVKTRRSRKXKSTLFOBELSKSOIVNVP---KRVGHAHTISIPLOTRMRECHQT	221	
QY	282	VKVSILFRVYRPRRRFNGMNGENTENIDVNEELPARRRNDEDEKTFVAQMTYFDK	341	
DB	222	L-VKTLFRK-----	VLSPSTCN--DENNETPP-NKRSHPN-EKMFSSLLIYEK	266
QY	342	NRRLQLDGEYEVAMQMEBCPI---SKKATWETIIDGKRLP---PFETFSQPTIQT	395	
DB	267	SSGP-ITEGEYEAALQPLNSTSIKSPKCTWETMPD-SYIPLSLTYDVYQOSPMKLFH	324	
QY	396	LKWTGENDKSTAPIALPLATR-----NSESILHOEN-----KPGSVKPTQTI	437	
DB	325	LTL---SNEOLPEMISAPELQRYVYOHDAVAEMNNYNNNNNNNCGSLKNGSGGNSGV	381	

Qy	438	AVKSLTITDLOQRKKEKDPENRQKRLRYEOPFLYNNNTQOQTEARBDLHCPCWTLNCRKX	497
Db	382	C-----KTP-----EHIQIYNNPYSNNITQOQTEYTOELNCPWGLDCLRKX	423
Qy	498	YSLKHLKLCRSHFIFENYVYHFKGARIDVINECYGSAVNPQDHRQGFAPFSBN-GP	556
Db	424	YALLHLKLCRHFNFYQYQAGSGARIDVTINDAYDGSVAGSPYDLAGRSGSSFAFTCCG	483
Qy	557	VKRPITHLVCRPKTKASMSGFELESDGEVEOQRTYSSGHNRLYFHSDTCLPLRQEM	616
Db	484	VKRTSVTSILMWCRRPROKCLDEPFLDEDEISNORSYITGHNRLYHMTETCLPHAPKEL	543
Qy	617	EYDSEDEKDEPWLREKTTIQIIEFSPVNSGEKVMKMLYHVKHGFIADNQNHHCMLE	676
Db	544	DIDSGESDPLMLRQKTIOMIDEFVSVNGBEKEMLKMLYHVRHGFVGQCOPLIACENP	603
Qy	677	VENYEQKIIKKNLCENFMHLVSMEDFNLSIMSIDKAYTKLREMOOKLEKES-----	730
Db	604	LDAKTEIVRKULYNNFILHMCSLPRFYGIILAEYVKYQKLGILLSKYAAGELMQROR	663
Qy	731	-----ASPANEITE-----	740
Db	664	EEQLKVMYLDVGMHKKQOEDPKTLKSPQKAPAPADQASTSASTSGSGSSSMQPPKRMPA	723
Qy	741	-----EONGTANGFSEINSKEKALETDSVSGVSKQSKQKL	776
Db	724	HLKRGSAASSPGVQSGKTENGNGSNS-----SSNSKUVAKKSSAOPPL	767

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RESULT 2
US-09-270-767-60845
; Sequence 60845, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-054
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60845
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60845

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[illegible][illegible]

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RESULT 3
US-10-144-198-16
; Sequence 16, Application US/10144198
; Patent No. 6833247
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 105 R1
; CURRENT APPLICATION NUMBER: US/10/144,198
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 243
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
US-10-144-198-16

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Query Match          16.2%: Score 661; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,46-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 MTGIAAAFFSNTCGFGCGGLHPTLADLIIEHIEDNHIDTPRVLKQELQOPTVVALSY 60
DB      1 MTGIAAASFNSNTCRFGCGGLHPTLADLIIEHIEDNHIDTPRVLKQELQOPTVVALSY 60

QY      61 INRFMTDARAREOBESLKKKIQPKSLTSLSSVSRRGNVSTPPRHSSGSLTPVTPETPS 120
DB      61 INRFMTDARAREOBESLKKKIQPKSLTSLSSVSRRGNVSTPPRHSSGSLTPVTPETPS 120

QY      121 SFRSSTPT 128
DB      121 SFRSSTPT 128

RESULT 4
US-10-104-047-2404
; Sequence 2404, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:

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;; PRIOR FILING DATE:
;; NUMBER OF SEQ ID NOS: 4096
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2404
;; LENGTH: 243
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-104-047-2404

Query Match 16.2%; Score 661; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAAASFPSNTCRFGCGGHHPTLADLIEHIEDNHIDTPRVLEKQELQOPTYVALSY 60
DB 1 MTGIAAASFPSNTCRFGCGGHHPTLADLIEHIEDNHIDTPRVLEKQELQOPTYVALSY 60
QY 61 INREMTDAARREOSLKKKIOPKLSLTLSVSVSRGNVSTPPRHSSGSLTPPVTPPTPSS 120
DB 61 INREMTDAARREOSLKKKIOPKLSLTLSVSVSRGNVSTPPRHSSGSLTPPVTPPTPSS 120
QY 121 SFRSSTPT 128
DB 121 SFRSSTPT 128

RESULT 5

US-09-513-999C-7263
;; Sequence 7263, Application US/09513999C
;; Patent No. 6783961
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Duclert, A.
;; APPLICANT: Giordano, J.Y.
;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;; Patent No. 6783961
;; FILE REFERENCE: 59, US2, REG
;; CURRENT APPLICATION NUMBER: US/09/513, 999C
;; CURRENT FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/122,487
;; PRIOR FILING DATE: 1999-02-26
;; NUMBER OF SEQ ID NOS: 36681
;; SOFTWARE: Patent.pm
;; SEQ ID NO 7263
;; LENGTH: 102
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 27
;; OTHER INFORMATION: Xaa=Ala or Asp
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 32
;; OTHER INFORMATION: Xaa=His or Asn or Arg or Ser
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 36
;; OTHER INFORMATION: Xaa=Asp or Asn
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 41
;; OTHER INFORMATION: Xaa=Asp or Gly
;; NAME/KEY: UNSURE
;; LOCATION: 79
;; OTHER INFORMATION: Xaa=Lys or Thr
;; NAME/KEY: UNSURE
;; LOCATION: 83
;; OTHER INFORMATION: Xaa=Lys or Arg
;; FEATURE:
;; NAME/KEY: UNSURE

;; LOCATION: 89
;; OTHER INFORMATION: Xaa=Ser or Tyr
US-09-513-999C-7263

Query Match 10.7%; Score 437.5; DB 2; Length 102;
Best Local Similarity 89.1%; Pred. No. 5e-33;
Matches 90; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 MTGIAAASFPSNTCRFGCGGHHPTLADLIEHIEDNHIDTPRVLEKQELQOPTYVALSY 60
DB 1 MTGIAAASFPSNTCRFGCGGHHPTLADLIEHIEDNHIDTPRVLEKQELQOPTYVALSY 60
QY 61 INREMTDAARREOSLKKKIOPKLSLTLSVSVSRGNVSTPPRHSSGSLTPPVTPPTPSS 100
DB 61 INREMTDAARREOSLKKKIOPKLSLTLSVSVSRGNVSTPPRHSSGSLTPPVTPPTPSS 101

RESULT 6

US-09-339-947A-8
;; Sequence 8, Application US/09339947A
;; Patent No. 6630616
;; GENERAL INFORMATION:
;; APPLICANT: YOSHIDA, No. 6630616umasa
;; APPLICANT: YANAI, Yukihiko
;; APPLICANT: KATO, Yoshihiro
;; APPLICANT: HIRATSUKA, Junzo
;; APPLICANT: TAKAHASHI, Shigeru
;; APPLICANT: MIYA, Tatsushi
;; TITLE OF INVENTION: GENE FOR FLORAL REGULATION AND METHODS FOR CONTROLLING
;; FILE REFERENCE: 032735-001
;; CURRENT APPLICATION NUMBER: US/09/339, 947A
;; CURRENT FILING DATE: 1999-06-25
;; PRIOR APPLICATION NUMBER: JP 1998-180065
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: JP 1999-179043
;; PRIOR FILING DATE: 1999-06-24
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 8
;; LENGTH: 604
;; TYPE: PRT
;; ORGANISM: Oryza sativa
;; FEATURE:
;; NAME/KEY: ZN PING
;; LOCATION: (310)..(335)
US-09-339-947A-8

Query Match 5.8%; Score 238.5; DB 2; Length 604;
Best Local Similarity 18.9%; Pred. No. 3.9e-13;
Matches 130; Conservative 95; Mismatches 242; Indels 221; Gaps 22;

QY 129 EPTGIYRFLRTNLIADIFLHRTLYNSH--RNSRTNI-----KRTFKVDDMLSKVE 179
DB 27 KPVELVNIQRRSIKNDPAFLORCLLYKHARRKRSILITLSGCTNKELRQAQIFPLVY 86
QY 180 KMKGEQESHLSAH-----LQITGTFPKNDKPS---PNSN--EQNSVTLAV 223
DB 87 LLARPTNVSLBGSPIYRPSRACLTSFHEFGKDYTAATPVLPDVKNATSRACSLNI 146
QY 224 LVVVCVHKRR--DVSCPIROYPTGKQ-----VLPVLDLQOTKGNPPLAVS 270
DB 147 ILIS-CGRAQOTPDNNCSGNHYBGLTQLGKGCFFGKIPI--DLAASSLGNVSL- 202
QY 271 SNEFEPNSHMVXSYSLFVTRPGRRFNGMNGETNENIDVNEELPA--RRKRNEDG 328
DB 203 -----GHTVMSSTVEMTPSFLPKFLBDS 228
QY 329 EKTIVAGMTVPDDKRRPLQLLDGEYVAMQEMECPIISKRAATWETIILDGRLPPFFTFSSQ 388
DB 229 CLTFCSQKVDATGSPLOVSIISAQEGAKQMSSPYS-----VYSYNDVPP----- 274
QY 389 GPTLQFTLRWTGETNDKSTAPIAKPLATRNSESLHGENKPGSVKPTQTIIVKSLTTDLQ 448

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Db 275 -----S$LH$IR 282
OY 449 TRKEKDTPENENOKLRIFYQPLYNNTROOTEARDDLHCPEWCTLNCRLYSLKHKLCH 508
283 LRSQ-----NVLBNYKXNNYNTWOTKTEVEDPFCBFCILVPCGSEFKGLCHNASH 331
OY 509 SRFIENYVYHPKGARIDVSI-NECVGYSVAGNQDILHRQBGFA$BNGP$KRTPIP- 563
332 DLFIHEFWI$ECCOAVN$SLKTD$MTELLAB$VDRPHQTSFYRSR$FKK$K$RVEI$SDKI 391
OY 564 ----H$WVC-RPKRTKASWSEFLSEDEVEQOITYSGH----- 598
392 RHVH$HIVDSGSPEDAQ$-----SEDDYVGGENGSSVAH$ASVDPAN$LSH$NLSAPV 445
OY 599 -----NRIYFS$D$TLPI$RQEM--EVD$SEKDP$EM$REKT 633
446 LQFGKTRKL$VERADPRN$OLLQKQF$H$HRAQ$PAM$S$VFS$DR$SEB$VDD$DIAD$FED 505
OY 634 ITQIEE$P$D$V$N$GEKE$V$M$K$NL$H$V$K$H$G$FIAD$N$M$H$A$C$M$L$F$V$ENY$G$Q$K$IL$K$N$L-----C 690
506 RRM$D$F$V$D$T$DEK$L$I$M$M$M$N$S$F$V$K$Q$V$L$AD$G$H$I$P$M$A$E$A$S$Q$H$G$E$L$V$Q$N$P$LL$W$C 565
OY 691 RNF$M$L$H$V$M$D$F$N$L$I$S$M$S$I$D$K$A$Y$K$L 718
566 W$F$F$--M$Y$G$L$M$H$S$L$I$D$A$R$A$M$A$C$N$T$I$L 591

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RESULT 7
US-09-339-947A-1
/ Sequence 1, Application US/09339947A
/ Patent No. 6630616
/ GENERAL INFORMATION:
/ APPLICANT: YOSHIDA, No. 6630616umaba
/ APPLICANT: YANAI, Yukihito
/ APPLICANT: KATO, Yoshihiro
/ APPLICANT: HIRATSUKA, Junzo
/ APPLICANT: TAKAHASHI, Shigeru
/ APPLICANT: MIWA, Tatsushi
/ TITLE OF INVENTION: GENE FOR FLORAL REGULATION AND METHODS FOR CONTROLLING
/ TITLE OF INVENTION: FLOWERING
/ FILE REFERENCE: 032735-001
/ CURRENT APPLICATION NUMBER: US/09/339,947A
/ CURRENT FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: JP 1998-180065
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: JP 1999-179043
/ PRIOR FILING DATE: 1999-06-24
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 611
/ TYPE: PR1
/ ORGANISM: Arabidopsis thaliana
/ FEATURES:
/ NAME/KEY: ZN_P1NG
/ LOCATION: (306)..(327)
US-09-339-947A-1

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	Query Match	5.5%;	Score 224;	DB 2;	Length 611;
	Best Local Similarity	19.1%;	Pred. No. 96-10;		
	Matches 132;	Conservative 102;	Mismatches 252;	Indels 206;	Gaps 23
OY	EPTQYRFLRTNLAPILFHLTLYMSHRNRTNIKRTKEFYVDDMLSKVECKGBQESH	188			
	: : : : : : : : : : : : : : : :				
Db	KPEVLINIQRRAIRNPFLQRCLEHYKI EAKKKRRIQMTVP-	70	-SG		
OY	SISALQLTTGTFHKKDKSPNSEQNSTVLELVAVCHKKRDVSCPIRQ-----	242			
	: : : : : : : : : : : : : : : :				
Db	71 AIDAGVQ-----TQLPFLYLITLRLATLSPK-----PVAEYSAYVR	105			
OY	243 -----VPPGKKOVP-----LIPLDLN-----QTQPGN-----PSGLAVSNSEFEPSNSH	280			
	: : : : : : : : : : : : : : : :				

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Db 106 FSRACILGGLGVDSQAQANFLPDMNNRLALEAKSGSIALTLFSPAGAQNSQFEDBSG 165
Qy 281 WVKSYSLFVTRPGRREFGNGINGENTENIDNEELPARRRKRNDEKTVVAQMTVPD 340
Db 166 KIH$-----NIGGHC-----LMSKIPLQ-----SLYASWQ 191
Qy 341 KNRLQQLLDGEYVAMQMEBCPI$KKAATWETLIDGRLLPFFFTFSQGPLOFTLRWG 400
Db 192 KSPNNDLQQRVDVTVSLVEMOPCFIKLKMSEKCS-----IQVPSNPLT----- 236
Qy 401 ETNDKSTAPILAKPLATRNSESI$HOENKCGSVKPTQI$AVKESJTLTIDLQTRKEDOTPENNR 460
Db 237 -----SSSPQOVQVIT$ABEVG$TEKSYSSSTYNDIS-SSSLDQITLR----TGN--- 283
Qy 461 QKRLFYQFOLYNNNTROQTEARDDLHC$PWLCLNCRKLYSL$KHLKLC$HSRPIENYVYHPK 520
Db 284 ----VFNRYRYNNKLQKTEVTEDEP$CFCFLYKCA$FGLR$HLPSTHDLNLFEEFVTEB 339
Qy 521 GARLDV$INECYDGSYAGNPODIH-RQ$GFAF-----SRNG----- 556
Db 340 FOAVNVSLKTEMT$ISKV-NEDDVDPKOOTFF$SSKKFRRRROK$QVRS$ROGPHLAGE 398
Qy 557 -VKRPIPHILLVCRKR-----TKA 575
Db 399 VLDKTDDAH$VRSSEKSRILP$GKHRYERIGAGBSGQVPRP$GTSADVQSCGDPDYVQSIAGS 458
Qy 576 SMS$FLESDESEV$EQ--RTYSSG$NRL$YFHS$DTC$PLRPO$M--EVDSEDEKDEMLRE 631
Db 459 TMLQ$PAKTRKISIE$SDLRKNSLQKQ$FPHSHRQ$P$ALBEV$LDRB$SEDEVD$DVA$F 518
Qy 632 KTIQOIE$FSDVNE$G$E$VKML$ML$V$K$GFIADQ$M$N$HACMLFVENY$GOKI$K-KNLC 690
Db 519 EDRRLMDL$FVDVTVTK$Q$K$M$M$M$M$N$S$F$V$K$Q$V$T$AD$GHI$P$WAC$EAF$SRL$H$GPI$M$V$R$PHLI 578
Qy 691 RNFM$IL$V$M$D$FN$IL$M$S$IDK$AVT$K$R$EMQ 722
Db 579 WCMR$F$V$N$V$K$L$M$N$H$G$L$D$A$R$Y$M$N$C$N$T$P$LE$O$LQ 610

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RESULT 8
US-09-270-767-44285
; Sequence 44285, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44285
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44285

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[illegible]

QY 266 SLAVSSNEP-SNSHMYKSYLLFRVTRPGRREFNGMNGTENNIDVNEELPARRKN 324
Db 175 TISILQTRPMGEQHTL--YKLLFRK-----VLSPTCN--DENATPP-NRKS 220
QY 325 REDGKTFVAMQTVFDKN 342
Db 221 RPN-EKMFSEILLYEKS 237

RESULT 9

US-09-750-590A-2
; Sequence 2, Application US/09750590A
; Patent No. 6780987
; GENERAL INFORMATION:
; APPLICANT: Herman, Ira
; APPLICANT: Welch, Alice
; TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL AND
; FILE REFERENCE: TUI-001CP
; CURRENT FILING DATE: 2000-12-28
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/170,182
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/733,818
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1401
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-750-590A-2

Query Match 3.9%; Score 160; DB 2; Length 1401;
Best Local Similarity 18.8%; Pred. No. 3.4e-05;

Matches 135; Conservative 139; Mismatches 285; Indels 160; Gaps 30;

QY 36 NHIDDP--VLEKQELQOPTYVALSYINRMTDAARBOESLKKIOPKSLTSSSV 92
Db 719 NNLTTEMKNVPLKVEEMKSHDVAVDLNTKSLSVTHKYTE--KLEMEKLMENASL 775
QY 93 SRGNVS-----TPRHSSG--SLTPPVTPITPSSFRSSTPTEPTQIYRFLTRNLI 143
Db 776 SK-NVSRLETWFIPERHEKEMALKSNITELKQSLSEKKGDEKIVSLMSENNDL 834
QY 144 APIFLHRLTYMSHNSNTNKKRTFYDDMLSKYERKKGDESHSLNHLQLTGTGFH 203
Db 835 KKTMSHQVVPVKTHEITLSTLDTKTNRELVDVK-KCED-----INQEFVKIKD 885
QY 204 KNDKPSSENEONSVTLEVLVVKYCHKKRDVSCPIROVPTG-----KKQVPLPD 255
Db 886 ENELIKRLLENTQNVKAEYISLRHEKMSGLRSMKKVQDNGSAEILAKYKSGBEIYT 945
QY 256 LNQTKPGNPSLAVSSNEFEPNSHMYKSYLLF-----RVTRRGRREFNGMNGTNE 309
Db 946 LHE-----EIAQKRELDTQECIKLKVAPIISLECEKFKATEKELKQSLQOTOK 998
QY 310 NIDVNEELPARRKGRDEGKTFVAMQTVFDK-----NRRLQLL 348
Db 999 YNTSEEEKKCKQENDKLLKELLTLQKDKKNVHIENSYETERALSRKTEELNQLKDL 1058
QY 349 DGEYEVANQMEBECPSISKRAIWE-----TILDGRLLPPEFTFSGPTLQFLRWGTEN 403
Db 1059 LQKTEAKGEKEKVLVEBAKQISELLAQTLQKQHP-----LEQVESLKSLSTIET 1113
QY 404 DKSTAPLAKPLATRNS-----ESLHQENKPGSVKPTQTIIVAKESITLTL 447
Db 1114 -----LKEELKTKQRCYEKEQOVTQRLQMLENQNSSVPLAEHLQVKEAFBKVGIIIX 1167
QY 448 OTRKEKOTPNENR-----OKRIIFYOFLYNNNRQ-----OTIARD-----DLHCP 488
Db 1168 ASLRKEBESQNKTEEVSKLOSEIQ-----NTKQALKLLETRVVDLSKRYKATYSDLTQ 1222

QY 489 WCLNCRKLYSL-LKHLKLCBSRFIFENYVYHPKGRIDVINSINECYDGSVAGNPQDIHOP 547
Db 1223 ISDNL-EXLANINRKYEVCEE-----VLHAK--KKGLSADKDELLHFSIEGELXQO- 1272
QY 548 GPASRNGPVKRTPTTHLVCPKTKASMSFLESED-----GEVQOQRTYSSGNR 600
Db 1273 -----QERCKSLITTEL-----QRIQESAKQ-IEAKNKITTELLNDVRLKQALNGLSQ 1323

RESULT 10

US-08-755-587-186
; Sequence 186, Application US/08755587
; Patent No. 6045397
; GENERAL INFORMATION:
; APPLICANT: Futreal, Phillip A
; APPLICANT: Wooster, Richard F
; APPLICANT: Ashworth, Alan
; TITLE OF INVENTION: Materials and methods relating to the
; TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson
; STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
; CITY: Raleigh
; STATE: NC
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,587
; FILING DATE: 25-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9523959.6
; FILING DATE: 23-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525555.0
; FILING DATE: 14-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9617961.9
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-135
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-755-587-186

Query Match 3.9%; Score 159; DB 2; Length 1494;
Best Local Similarity 18.3%; Pred. No. 4.7e-05;

Matches 177; Conservative 151; Mismatches 355; Indels 284; Gaps 46;

QY 23 PPTLADLIEHIDNHDTPRVLKQELQOPTYVA-LSYINRMTDAARBOESLKKKIQ 81
Db 370 FKIASNKKEIKSENNIRKSKMLFROIIEHYPTNLACLEIYVTSLSQKPKSKS--HALD 427
QY 82 PKSLTILSSSVSRGNVTPRHSSGSLPPTPTITSSFRSSTPTEPTQI----- 133
Db 428 FOINI-ISGFVQ--NSTYVSDSSGHTAPPLSLKQDFSNRLTPQOKAIBELSTILE 484
QY 134 -----YRFLTRNLADIPLHRLTYMSHNSRT--NIKRTFYDDM-----LSKVE 179

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Db      485  ESGSGREFRFRK---PSHIQKNPMPENQTLINSTSEKEMKDDILHLTNAPSIQVD 541
Qy      180  KMK-----GEQSHSLSA-----HLQTLTFEFH-KNDKSPNE----- 213
Db      542  SKRSEGIIGKQKQFACLSRTSCNRASGVSTDKNEVEFRFGARGLKLVNGSEALOKAK 601
Qy      214  -----NEQSV-----TLEVLVVKCHGRKDVSCPIRQVTPGKKOV 251
Db      602  KLFPSDLNINEETSVEDRSFSSSKYNDVSMIQIECDKNNE-----PANKCR- 652
Qy      252  LIPDLNQTCKGNPPLSAVSSNEPEPSNHWKYSLLFR-----VTRPGRRENGM 302
Db      653  -----ILQNNIEMTDTIPEEYETYSYRANTENEGNQTDAGRNTCNSE 695
Qy      303  ING---ETNENIDVNEE---LPARRKKNREDGEKTPYAQMTVDKRRLOLDGEVE--- 353
Db      696  SDGSDSKDPTVYIHEBENGLPCTIDQNIID-----LKLFSQPMKEGNTQIKGSLDLC 749
Qy      354  VAMQMEBECPISSKKRATWETILDGKRLPPETP---SGGPTLOFTLRWGTETNDKSTAPLA 411
Db      750  LVKABETSHVTSNKKQTLANTGQNIKDPDTYLSQTSARKNIRVRESLANKASLILN 809
Qy      412  KPLATRN---SSSLHQENKRG-SVKPTQTIAYKESITTDLOTRKEXDT----- 455
Db      810  QKTEEBELNPFSDLSNSELPGIDIKTID---ISNHEVIENTERKOKITVESLIGTENIL 866
Qy      456  -----PNERQQLRTFYQPLVNNNTROQTEARDLHCPMCTANCRGLYSLHLGLCHS 509
Db      867  LILQORESKIKIKISAVLGFHTASGKLEITKE-----SLDVLKXNLFBEKQDONS 918
Qy      510  RFIENYVYHPKGRIDIVSINECYDG-SYAGNPODIHQPGFARNGPVKRTPIITHILVC 568
Db      919  E-ITNFSH--RGAKMSDRBCECKDGRGLACGTTRITTPTEYERTHSLEKKVYSNELAL 975
Qy      569  RP-----KRT-----KASMSFLESDEGE---VEQRTYSSGHNRLYFPH 604
Db      976  RPRLLSDNLKYQTEENLKISDHASQKVDVHENTETETAKKPTMYNQTYSALINSPITFT 1035
Qy      605  SDTCPLRPQPMEDVDEDE--KQPEMLREKTIQIEFSD---VNEGEKVMKMLNHLV 658
Db      1036  QDT-----BEKPSVESASLFEAKKMLRE-----GEMDQSERINAAKNCKEYPPDYV 1083
Qy      659  -----MKHGTADNOMNHACMLFVENYGOXTIHKKYLGRN-FMLHLVSMHD---FNLIS 707
Db      1084  ENPSCGSSSALTENDKXN---LSBKQSTYLSNSTMNSYSYHGFCHSSEVYVNXSE 1139
Qy      708  IMS-----IDKAVTKLREMO-----QKLEKGBSASP 733
Db      1140  YLSRSKIDNSGIBPVIKNIRERKNIGFSEIMSPGREADTPQGSVNDICVEKLATNSCKN 1199
Qy      734  AN-----EETEBQNGTANGFSEINKF-----KALE--TDSVSGVS 768
Db      1200  KNTAIKVAISDSNNFTIOKLNDSNNSVPAYSTVSKRVAVAHQTCTVTGFTDNCMTV 1259
Qy      769  KOSKQOK 775
Db      1260  KONTYKSK 1266
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RESULT 11
US-09-134-001C-5080
; Sequence 5080, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
```

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; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5080
; LENGTH: 3696
; TYPE: PR
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5080
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Query Match      3.8%; Score 156.5; DB 2; Length 3696;
Best Local Similarity 17.4%; Pred. No. 0.00035; Indels 189; Gaps 32;
Matches 140; Conservative 147; Mismatches 327;
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Qy      30  IEHIEDNHIDTPRVLEKQELQOPFYVALSYNRFMTDAARBOESLKKIOPKLSITLS 89
Db      1926  LKINNIQOSTQTKNAKQEIINDKAOEQLQINN--TPDTEEBEKQATNRVNAAGLAQIQ 1984
Qy      90  SSVSRGNVSTPRHSSGSLTPVTPPTPSSFSRSTPEPQIYRFRFLRNLIAPIFLH 149
Db      1985  -----NINN--AHSQEVNESKTSIATIKSVQPVVKKPVALINSITQEAN----- 2028
Qy      150  RUTLYTSHNSKRTNKKR-----TPKVDMLSKVEKMGQESHSLAH-----LOLTFT 199
Db      2029  NOKTLIGNDGNATDDEKEKAKQLVTQKLEQIQKIHSTQDQVQDVKAQAIYALKLI-- 2086
Qy      200  GFPHKNDKPSPNSENEQNSVTLLEVLVVKCHKKRQDVSCPIRQVPGKKQVPLIPDLNQT 259
Db      2087  -----NANAHRQQDAIN---ILTNLAEKSKDIRA--NQDATTEBKNTALIGSIDT 2132
Qy      260  KQGNFPLSAVSSNEPEPSNHWKYSLLFVTRPGRRENGMNG----- 305
Db      2133  -----LQARNNINIGANTNALVDENL-----EDGKQLORIVLSTQTKTOAKADIAQ 2180
Qy      306  -----ETNENIDVNEELPARRKNRE-----DQEKTFVQGMVFD--KNNRLQOLDGE 351
Db      2181  IGOQRSTIDQONQATTEKQZALERLNOETNGVNDIOALANQONTDKNNILETIRNV 2240
Qy      352  YEVAQMEBECPISSKKRATWETILDGKRLPPETFSQGPLT---QFTLRWGTETNDKSTA 408
Db      2241  EPIVIVKPRANELIRKKAQQTLLNQ-----NQDATLEKQALQKLEEVKNKALINQ 2292
Qy      409  PLAKPLATNSSLHOEN---KPGSVKPTQITA--VKSLLTDTLOTRKEXDTPNENRQK 462
Db      2293  QVSO--AHSNNQVKALENNGIAKISEVHPETIIRKNAKQIEBDDQS--QITITINN--- 2345
Qy      463  LRIFYQFLNNTTROQTEARDLHCPWCTLNCRKLYSLKHLKLSRFLFVNVYHPKGA 522
Db      2346  -----NKSTNEKSAID-----RVNAKIDAI-----NNITNATTT 2377
Qy      523  RIDVSINECYDGSYAGNPODIHQPGFARNGPVKRTPIITHILVCRPRTTASMSFLE 582
Db      2378  QL--VN--DAKNSGNTSISQILPETA-----VX-----TNALALASBAKNKAIINQ 2421
Qy      583  SEDGEVEQORTYSSGHNRLYFHSDTCLPLRPQMEVDSDEKQPEMLREKTIITQI----- 637
Db      2422  TPNAATAEBKEKANNKVDRL-----QEBADANILKATTTDEVENINIKN 2462
Qy      638  EERSDVNEGEKVMKMLNHLVWKHGTIADNOMNHACMLFVENYGOXTIHKKLCRNFMHL 697
Db      2463  QAVQNTINAVQVEYIKQONVKQNLQNET--DNQCK-----ITETPDATLEKKAENLQON 2516
Qy      698  V-----SMHDFNLISIMSIDKAVTKLREMOQKLEKESASPANEETIEEONGTANGF 749
Db      2517  VLTSTDELAINDVHNNEVQALDKAPKIEIVPQVSKRDVLAHQEAFNSGTQRIQEN 2576
Qy      750  SEINSEKALETDSVSGVSKQSK 772
Db      2577  QEATNEKTEALINKIQLNOAK 2599
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RESULT 12
US-09-710-279-3188
; Sequence 3188, Application US/09710279
```

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; Patent No.6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STRAPHLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU348005
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatencIn Ver. 2.1
; SEQ ID NO 3188
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-09-710-279-3188

```

Query Match	3.8%	Score 153.5	DB 2	Length 1279	
Best Local Similarity	17.5%	Pred. No. 0.00012			
Matches 141	Conservative 146	Mismatches 310	Indels 211	Gaps 35	

Qy	30	IEHIEDNHIDTDPVLEKQELQOPTYVALSYINREPMTDAAAREQESLKKKIQPKLSLTLS	89
Db	528	LEKINNIOPSTQTKTNAKQIINDKAQEQELIQINN--TPDATEEKEQATNRVAGLAQAIQ	586
Qy	90	SSVSKGNVSTPRPHSSGLTPPYPTPIPPSSFSSTPEPTPEQYRFLTRNLAPFLH	149
Db	587	-----NINN--AHSTQEVNESKTSIATIKSVQPNVIAKKPAINLSLQEAN-----	630
Qy	150	RTLTYMSHRNSRTNJKR-----TFKVDMDLSTYKKKKGEQESHLSAH-----LQTF	199
Db	631	NQKTLIGDGNATDEKKAQOLVTOKANEOQKIHSTEQDQNDVNAQOAITAKLT--	688
Qy	200	GFFHKDKPSPENSEQNSVTLVLVYVCHKKRQDVSCPIRQVPTGKQVPLIPDLNQ	259
Db	689	-----NANNAHKRQDAIN---ILVTIAESKKSDIRA--NQDATEEKNALIGSIDT	734
Qy	260	KPGNPSPLAVSSNEPEPSNSHWKYSISLFPTRTGRREPFNGMNG-----	305
Db	735	-----LAQARNNINGANTALVDEN-----EDGKKQKORIVLSTQTKQAKADIAQA	782
Qy	306	-----ETENIDIVNEELPARRKRNRE-----DGEKTPVAQMVFP--KXRLQDLG	351
Db	783	IGQORSTIDQONATTEKQELERLQNETNGCVNDRIQALALANQVDTBEKNILLETIRV	842
Qy	352	YEVANQMEBCPISKKRAITWETILDGKLPPEFTPSQGPUL--QFTLRMGETNDKSTA	408
Db	843	EPIVIVRKABEIIIRKKAQEQTLTINQ-----NQDATEEKGIALGKLEVNGEALN	894
Qy	409	PIAKPLATRNSESLSQEN---KPSVYPTQTLA--VESLTTDLQTKREKQDPNENQK	462
Db	895	QVSO--AHSNNDVKIVENNGIAKISEVHEPTIKKNAQOIEBDAQS--QIDTTNAN---	947
Qy	463	LRIYQFLYNNNTROQTEARDLDHCPWCLTNCRLKSLYLKHLKLSHSFIFNVYVHPKA	522
Db	948	-----NKSTNEKSAID--RANVAKDAI-----NNITANATT	979
Qy	523	RIDVSIINECYGSYAGNPDIHROGFAFSRNGPYKRTPTIHLIWCSPKRTKASMSFLE	582
Db	980	QL---VN--DAKSGNTSISQLIPSTA-----VK-----TNALALASEAKNKVALIDQ	1023
Qy	583	SEDEVEQQRYYSSGHNRLFYHSDICPLRQPEMEVSEDEKDEPMLEKTIITQ----	637
Db	1024	TPNATAEKEKEANNNVDRL-----QEEADANILAAHTTDEVNNIKN	1064
Qy	638	EEFSDVGEKGRVMGLAMLIHWKGFPIADNQNMTHACMLFVENYGGQIKI-----	686
Db	1065	QAVQNINNAVQYEVIVIKQN-----AKNQALNQ-----FINDQ--KTIETNPDATELEKA	1110
Qy	687	--KULCRNFMTLHL---VSMHDEPLNISIMSIDAKVTKLREMOQKLEKESGASPANEETEE	741

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Db      1111  EAMFLLOAVLTSTSD EIAINVHDHNEVDQALMKARPKLEAIVPQVSKRDALNALQEA FNS 1170
Qy      742   QNGTANGSEIINSKEKALETDSVSGSVK 769
Db      1171  QT-----QETQEKQEAFTNEKTEALNK 1192

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RESULT 13
US-09-248-796A-17551
Sequence 17551, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17551
LENGTH: 584
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-17551

Query Match          3.7%  Score 151.5; DB 2; Length 584;
Best Local Similarity 19.5%  Pred. No. 5.1e-05;
Matches 129; Conservative 84; Mismatches 201; Indels 249; Gaps 33;

61 RGRSHFNSQFQRMNRSRPVLLPSSRDNNNTTNP-----IPILPSTNSNNPITSS 113
70 RRQESLKKKTIQPKLS---LTLSSSVSRGNVSTPRHSSGSLTPPTP-----PITGS 119
120 SSFSSSTPTEPTQIYRFLRT--RNLAPIFLHRTLTYMSHRNSRTNKKRTPFVDMLSKV 178
114 SNSRWFSPNPSPLYPVVTTSPSALSPTQH-----HQOQOQLHKF-KTSSNGSNT 165
179 EKMKGQESHSLSAHL-----QLTFTGFPHKDKPSPNSEGNSVTLFVLLVKKVCHKKK 234
166 PITGGGIGSPSTTSYLSANISYR-----RSQPLKDNNGTSSSTTK----- 206
235 DVSCPIRQVPYGGKQVPLIPDLNQTGPGNFSPLAVSNF---FEPSSNHWKSYSLFR 250
207 -----DNNNT-----IIEEDQKFFLAKKALV----- 229
291 VTRPGRBREFNGINGETNEN---IDVNEELPARKRNEDEKTFPAQWTFVDKRRLOJ 347
230 ATAGGVKTNHNNNNCKFGNNTSKIDINNH--NKNNNKNSDGNET-ILDSITIDLRLQY 286
348 LDGEYVAMQEMEBCEPISKKRAWTETILLDKRLPEPEFSSQGPITQ---FTLRMTGETND 404
287 ASAPHGNPIGQISGLQNTSKGL-----LEVQDESNFPDIDNNNFVYNNNDNNN 336
405 KSTAPIAKPLATRNSESLHQR--NKEG-----SVKPTQ-----TTA 438
337 TTS-----NSKESNNYHPSGNEBPGWFFLDEASTKTSNTSTGTGTGIGATTNI 389
439 VKESITLTDLQTRKED-----TPENARQKRLRIYQGLYNNNTROQTEARD- 483
390 ISES-ESGLAKYKRESIANIINPSTTTSTTNKQ-----NNNTSSSTIKTRKY 436
484 -----DLHCFWCTLNCKRLYSLKHLKLCHSRFLTFNYYVHFKGARIDVSNICEYDGSYA 537
437 SQDETRKPPCDCKPMSPFRSSDLKRHEK-----QHL 467
538 GNPDIDHQPAPASRNGPVRTPITHI--LVCRKRTKASMSFEL-----E 582
468 TTPNIPQFCGKGPARKDALR---HIGTLCKKNNAKKLYTENENYLNSSQDDDAE 523

```


/ TELEPHONE: 207-363-0558
 / TELEFAX: 207-363-0528
 / INFORMATION FOR SEQ ID NO: 8:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 912 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-005-002C-8

Query Match 3.7%; Score 150; DB 1; Length 912;

Best Local Similarity 18.5%; Pred. No. 0.00015;
Matches 153; Conservative 126; Mismatches 287; Indels 260; Gaps 37;

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QY 65 MTDARREQESLKKIQLPRLSLTLSSVRGNVSTPPRSSGLTPPYTPPTPSSPRS 124
DB 3 MODAKKESYSMPK-----TSSPPPTPTNMQIPYQADPLQMGYTQ 45
QY 125 STPEPTQI--YRPLRTNLI--APIPLHRT-----LTYMSHRN-----SRTNIRKRTF 169
DB 46 APYLYPTQIPAYSF-----NMVNQNPY-HQSGSPHILPQNNINGSTNNNNINKKKW 100
QY 170 KYDDMLSKVEKKKGQESHSLSAHLQLTFGFFHKDK-----PSPNS-----E 213
DB 101 HSNGITNN-NGSSGNQANSSGSGMSYNSHTYHNYSNNH1PMMA5PNSG5NAGMKQT 159
QY 214 NEQN-----SVTLEVLIVKCHKRRKDVSCPIROVPTGKKQVPLIDLNQT 259
DB 160 NSSNGSSSATSPSYSSTNSSQYDLYKFDVTKLV-----LKENSNNLIQLPLF--INTT 213
QY 260 KFG-----NPSLAVSSNEPEPSN-----SHVKSYSLLFVTRPRGRREFNGM 302
DB 214 EAEFAAASVQREYELMKALNINSESLSSVEKSAHHHTKSHI-----PKHNE 264
QY 303 INGETN-ENIDVNEELPARKKRNREDGKTFVAQMTVPDKNRLQLDGEYEVANQEMEE 361
DB 265 VKETEGEEDADHDKKPHASKDAHELKKEKTEYK-----EDAKQDRNE 307
QY 362 CPISKRAWTETILDGKLPPEPESQGPFLQFLRMGTETNDKSTAPIA---KPLATR 417
DB 308 KYIQEPQATVLPVVDKKE--PEESVEEN-----TSKTS5PSP5PPAK5WSA1ASD 356
QY 418 NSESLHQRKPGSVKPTQTIAYKESLITTDLQTRKEKQTPENENRQKLIFYOFLYNNNTRO 477
DB 357 AIKSKQANRKTYSGSMVTKTPISGTTAGVSSTNMAATIGKSSPL-----LSK 405
QY 478 QTEARDLHCPWCTLNCRKLYSLHLKLCBSRFTFNVTYHPKARIDV5INECYDGSYA 537
DB 406 QPKDKKTYVPSTKGIPLG5IA--LRMC5PDPFISVLRNKDVENKIPVHSII----- 458
QY 538 GNPQDIHQPGAFSRNGPVKRTPIITHLVCRP-----KRTKASM----- 577
DB 459 --PRGIINRANICF-----MSSVLQVLLYCKPFIQVINVLSRNTNSRVGTSSCKLLDA 510
QY 578 -----SEPLESEDG--EVEQARTYSSGHNRLYFHSDTCLPLRQEMEVDS 621
DB 511 CLTWYKQPKDEYKFKFLFNADDAKTESDAKSKSKSPQHCATADAVKDEP----- 565
QY 622 DEKQDEMLREKTTIQIEE5SDVNEGEKEVAKMLNHLVMKH-----GFIADNQNMHA 672
DB 566 -----YKTLSTIPKFKDLQWGHDAE5FLTHLDQLHEELISAIDGLTNE----- 612
QY 673 CMLFVENYGOKIKKNCNLFNLHVSMM--D5NLISIM5DKAVTKLREMOQCLBKE 729
DB 613 ----IQNNMQ5INDQUL--KVF5IRNLSRGKAEF-----IKN5PRLKEHLEKY----- 656
QY 730 SASPANBEITEONGTANGFSEIN5KERALE5TDSV5GV5KQ5KKQK 775
DB 657 --GVINDSTEE-----NGMH5-----V5G55K5G5K5TK 683
  
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Search completed: April 7, 2006, 13:07:39
Job time : 52 secs

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:17:23 ; Search time 170 Seconds
(without alignments)
1907.268 Million cell updates/sec

Title: US-09-874-162a-8
Perfect score: 4078
Sequence: 1 MTGIAAASFNTCRFGCGG.....KALETDSVSGVSKQKQKL 776

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Published Applications AA Main:
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.dep:
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.dep:
4: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.dep:
5: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.dep:
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.dep:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4078	100.0	776	3	US-09-874-162a-8
2	3413	83.7	739	3	US-09-874-162a-5
3	3413	83.7	803	3	US-10-942-711-16
4	2043	47.1	388	3	US-09-764-864-931
5	1944	47.7	367	5	US-10-942-711-54
6	1497	36.7	289	3	US-09-764-864-911
7	1453	33.6	292	3	US-09-764-864-1369
8	1127.5	27.6	955	6	US-11-097-143-41697
9	919	22.5	175	3	US-09-764-864-1355
10	661	16.2	243	3	US-09-874-162a-2
11	661	16.2	243	4	US-10-144-198-16
12	661	16.2	243	4	US-10-104-047-2404
13	652	16.0	278	3	US-09-764-864-1334
14	476	11.7	143	3	US-09-764-864-884
15	359	8.8	69	4	US-10-029-386-28495
16	280	6.9	171	4	US-10-276-774-2060
17	236	5.8	735	4	US-10-425-115-276256
18	226.5	5.6	626	5	US-10-739-930-6320
19	224	5.5	767	6	US-11-097-143-1512
20	221	5.4	440	5	US-10-739-930-6330
21	221	5.4	445	5	US-10-942-711-2
22	217	5.3	440	5	US-10-942-711-5
23	214.5	5.3	813	4	US-10-231-778-2
24	211	5.2	692	4	US-10-177-478-6
25	210.5	5.2	481	4	US-10-425-114-54921
26	205.5	5.0	640	4	US-10-437-963-193525
27	199.5	4.9	435	4	US-10-425-114-46823

28	195	4.8	635	4	US-10-425-115-256141	Sequence 256141,
29	192.5	4.7	428	4	US-10-424-599-254264	Sequence 254264,
30	184.5	4.5	598	4	US-10-425-115-276234	Sequence 276234,
31	178	4.4	298	4	US-10-425-115-276278	Sequence 276278,
32	176.5	4.3	1142	4	US-10-369-493-1700	Sequence 1700, Ap
33	176.5	4.3	1142	4	US-10-618-581-10	Sequence 10, Appl
34	175	4.2	1349	4	US-10-618-581-16	Sequence 16, Appl
35	170.5	4.2	1396	5	US-10-732-923-2883	Sequence 2883, Ap
36	161.5	4.0	583	4	US-10-451-467A-412	Sequence 412, Ap
37	156.5	3.8	3696	4	US-10-724-972A-5942	Sequence 5942, Ap
38	155.5	3.8	1328	4	US-10-083-357-1345	Sequence 1345, Ap
39	153.5	3.8	3692	4	US-10-282-122A-71235	Sequence 71235, A
40	152	3.7	1322	4	US-10-083-357-1332	Sequence 1332, Ap
41	152	3.7	1957	4	US-10-369-493-2070	Sequence 2070, Ap
42	152	3.7	1957	5	US-10-732-923-3328	Sequence 3328, Ap
43	151	3.7	1881	4	US-10-032-585-7646	Sequence 7646, Ap
44	150	3.7	912	4	US-10-369-493-1772	Sequence 1772, Ap
45	149.5	3.7	1015	5	US-10-732-923-3329	Sequence 3329, Ap

ALIGNMENTS

RESULT 1
US-09-874-162a-8
; Sequence 8, Application US/09874162A
; Patent No. US20020155452A1
; GENERAL INFORMATION:
; APPLICANT: Koontz, Jason
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZ1 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024001
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-162a-8

Query Match	100.0%;	Score 4078;	DB 3;	Length 776;
Best Local Similarity	100.0%;	Pred. No. 7.3e-309;		
Matches 776;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				
QY	1	MTGIAAASFNTCRFGCGGHPPTLADLIEHIEDNHTDTPRVLEKELQOPTVALSY	60	
DB	1	MTGIAAASFNTCRFGCGGHPPTLADLIEHIEDNHTDTPRVLEKELQOPTVALSY	60	
QY	61	INRFMTDAREOBSLKKKIQPKLSTLSSSVSRGNVSTPPHSSGSLTPPTPTPSS	120	
DB	61	INRFMTDAREOBSLKKKIQPKLSTLSSSVSRGNVSTPPHSSGSLTPPTPTPSS	120	
QY	121	SFRSTPEPQIYRFLTRNLAPIFLHRTLTYSHNSRTNIRKTKFYKDDMLSKYEK	180	
DB	121	SFRSTPEPQIYRFLTRNLAPIFLHRTLTYSHNSRTNIRKTKFYKDDMLSKYEK	180	
QY	181	MKGEOESHLSAHLQLTFTGFHNDKSPKSEKNQSVTLLEVLVKKCHKKRXOVSCPI	240	
DB	181	MKGEOESHLSAHLQLTFTGFHNDKSPKSEKNQSVTLLEVLVKKCHKKRXOVSCPI	240	
QY	241	ROVPTGKKQVPLIDNLQTKDGNFPLAVSSNEFSPSHVKSYSLLFRVTRPGRRFN	300	
DB	241	ROVPTGKKQVPLIDNLQTKDGNFPLAVSSNEFSPSHVKSYSLLFRVTRPGRRFN	300	
QY	301	GMINGETNENTDVNEELPARKKRNREDEKTFVQMTYFDQNRRLQLLDGSEYVAMQME	360	
DB	301	GMINGETNENTDVNEELPARKKRNREDEKTFVQMTYFDQNRRLQLLDGSEYVAMQME	360	

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Qy 361 ECPISKRAWTETILLDGKLPPEPETSOGPTLOFTLWGTENDKSTAPIAKPLATRNSE 420
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Db 361 ECPISKRAWTETILLDGKLPPEPETSOGPTLOFTLWGTENDKSTAPIAKPLATRNSE 420
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Qy 421 SLHQENKPGSVKPTQTITAVKESITTDLOTRKEKOTPNENRQKLRIFYOPLNNNTROOTE 480
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|
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Db 421 SLHQENKPGSVKPTQTITAVKESITTDLOTRKEKOTPNENRQKLRIFYOPLNNNTROOTE 480
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Qy 481 ARPDLCPCPOTNCRKLYSLKHLKICHSRPIFNYYVHPGARIDVSNCECYGSYAGNP 540
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|
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Db 481 ARPDLCPCPOTNCRKLYSLKHLKICHSRPIFNYYVHPGARIDVSNCECYGSYAGNP 540
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Qy 541 ODHRPGFAFSAFNGPVKRTPIITHILVCRPKRTKASNEFLESEDEVEOQRTYSSGHR 600
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|
|
Db 541 ODHRPGFAFSAFNGPVKRTPIITHILVCRPKRTKASNEFLESEDEVEOQRTYSSGHR 600
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Qy 601 LYHSTOTCLPLRQEMEVDSDEKDPMLREKITTQIEEFSDVNEGEKEVMKLMNLMHWK 660
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Db 601 LYHSTOTCLPLRQEMEVDSDEKDPMLREKITTQIEEFSDVNEGEKEVMKLMNLMHWK 660
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Qy 661 HGFIADNOMNHCMLFVENYGOKIKKNLCRNFMHLVSMHDFNLISIMSIDKAVTKLRE 720
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Db 661 HGFIADNOMNHCMLFVENYGOKIKKNLCRNFMHLVSMHDFNLISIMSIDKAVTKLRE 720
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Qy 721 MOCKLEKGSASPANEITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 776
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Db 721 MOCKLEKGSASPANEITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 776
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RESULT 2
US-09-874-162a-5
; Sequence 5, Application US/09874162a
; Patent No. US20020155452a1
; GENERAL INFORMATION:
; APPLICANT: Koonitz, Jason
; APPLICANT: Sklar, Jeffrey
; TITLE OF INVENTION: FUSION OF JAZZ1 AND JAZZ2 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874,162a
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-162a-5
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Query Match 83.7%; Score 3413; DB 3; Length 739;
Best Local Similarity 99.8%; Pred. No. 5.1e-257;
Matches 647; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 129 EPTQIRFLRTNRLAPIFLHRTLTYMSHRNSRTNKRKTFKYDDMLSKYKKKKGQESH 188
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Db 92 KPTQIRFLRTNRLAPIFLHRTLTYMSHRNSRTNKRKTFKYDDMLSKYKKKKGQESH 151
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Qy 189 SLSAHLQTLFTGFFHNKDRSPNSSENEQNSVTLEVLVVCYCHKRQDVSCPIRQVPTGKK 248
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|
|
Db 152 SLSAHLQTLFTGFFHNKDRSPNSSENEQNSVTLEVLVVCYCHKRQDVSCPIRQVPTGKK 211
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Qy 249 QVPLIDNLNQTGKGNFSLAVSSNEPEPNSHWKYSYSLFRVTRPGRREFNGMINEGN 308
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|
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Db 212 QVPLIDNLNQTGKGNFSLAVSSNEPEPNSHWKYSYSLFRVTRPGRREFNGMINEGN 271
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Qy 309 ENIDVNEELPARKRNRDEDEKTFVAQMTVPDKNRLQLLDGEYEVAMQEMECPSISKR 368
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Db 272 ENIDVNEELPARKRNRDEDEKTFVAQMTVPDKNRLQLLDGEYEVAMQEMECPSISKR 331
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Qy 369 ATWETILLDGKRLPPEPETSOGPTLOFTLWGTENDKSTAPIAKPLATRNSESLHQENK 428
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Db 332 ATWETILLDGKRLPPEPETSOGPTLOFTLWGTENDKSTAPIAKPLATRNSESLHQENK 391
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Qy 429 GSVKPTQTITAVKESITTDLOTRKEKOTPNENRQKLRIFYOPLNNNTROOTEARDDLHCP 488
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|
|
Db 392 GSVKPTQTITAVKESITTDLOTRKEKOTPNENRQKLRIFYOPLNNNTROOTEARDDLHCP 451
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Qy 489 WCTLNCRKLYSLKHLKICHSRPIFNYYVHPGARIDVSNCECYGSYAGNPQDHRQ 548
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|
|
Db 452 WCTLNCRKLYSLKHLKICHSRPIFNYYVHPGARIDVSNCECYGSYAGNPQDHRQ 511
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Qy 549 FAFSRNGPVKRTPIITHILVCRPKRTKASNEFLESEDEVEOQRTYSSGHRNLYFHSDFC 608
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|
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Db 512 FAFSRNGPVKRTPIITHILVCRPKRTKASNEFLESEDEVEOQRTYSSGHRNLYFHSDFC 571
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Qy 609 LPLRQEMEVDSDEKDPMLREKITTQIEEFSDVNEGEKEVMKLMNLMHWKHGFIADNQ 668
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Db 572 LPLRQEMEVDSDEKDPMLREKITTQIEEFSDVNEGEKEVMKLMNLMHWKHGFIADNQ 631
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Qy 669 MNHACMLFVENYGOKIKKNLCRNFMHLVSMHDFNLISIMSIDKAVTKLREMOQKLEK 728
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Db 632 MNHACMLFVENYGOKIKKNLCRNFMHLVSMHDFNLISIMSIDKAVTKLREMOQKLEK 691
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Qy 729 EGASPANEITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 776
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Db 692 EGASPANEITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 739
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RESULT 3
US-10-942-711-16
; Sequence 16, Application US/10942711
; Publication No. US20050132446a1
; GENERAL INFORMATION:
; APPLICANT: Dean, Caroline
; APPLICANT: Gendall, Anthony
; TITLE OF INVENTION: Methods and means for modification of plant characteristics using
; FILE REFERENCE: Mewburn
; CURRENT APPLICATION NUMBER: US/10/942,711
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US/09/890,220
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/GB00/00248
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: GB 9901927.5
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-942-711-16
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Query Match 83.7%; Score 3413; DB 5; Length 803;
Best Local Similarity 99.8%; Pred. No. 5.8e-257;
Matches 647; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 129 EPTQIRFLRTNRLAPIFLHRTLTYMSHRNSRTNKRKTFKYDDMLSKYKKKKGQESH 188
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Db 156 KPTQIRFLRTNRLAPIFLHRTLTYMSHRNSRTNKRKTFKYDDMLSKYKKKKGQESH 215
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Qy 189 SLSAHLQTLFTGFFHNKDRSPNSSENEQNSVTLEVLVVCYCHKRQDVSCPIRQVPTGKK 248
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Db 216 SLSAHLQTLFTGFFHNKDRSPNSSENEQNSVTLEVLVVCYCHKRQDVSCPIRQVPTGKK 275
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Qy 249 QVPLIDNLNQTGKGNFSLAVSSNEPEPNSHWKYSYSLFRVTRPGRREFNGMINEGN 308
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Db 276 QVPLIDNLNQTGKGNFSLAVSSNEPEPNSHWKYSYSLFRVTRPGRREFNGMINEGN 335
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Qy 309 ENIDVNEELPARKRNRDEDEKTFVAQMTVPDKNRLQLLDGEYEVAMQEMECPSISKR 368
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Db 336 ENIDVNEELPARKRNRDEDEKTFVAQMTVPDKNRLQLLDGEYEVAMQEMECPSISKR 395
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QY 369 ATWETLLDGRKLPPEFTPSGGPTLQFTLWGTSTNDKSTAPIAKPLATNSSESLHQENK 428
 DB 396 ATWETLLDGRKLPPEFTPSGGPTLQFTLWGTSTNDKSTAPIAKPLATNSSESLHQENK 455
 QY 429 GSVKPTQTAVKESLTTDQTRKEKTPPENRQKLI FYQFLYNNNTROOTEARDLHCP 488
 DB 456 GSVKPTQTAVKESLTTDQTRKEKTPPENRQKLI FYQFLYNNNTROOTEARDLHCP 515
 QY 489 WCTLNCRKLYSLKHLKLGHSRPIFYVYVHPKCARIDVSNCEYDGSYAGNPODIHROP 548
 DB 516 WCTLNCRKLYSLKHLKLGHSRPIFYVYVHPKCARIDVSNCEYDGSYAGNPODIHROP 575
 QY 549 FAFSRNGPVKRTPTITILVCRPKRTASMSSEFLSEDEGEVQRTYSOGHNLRYFHSDDC 608
 DB 576 FAFSRNGPVKRTPTITILVCRPKRTASMSSEFLSEDEGEVQRTYSOGHNLRYFHSDDC 635
 QY 609 LPLRPOEMEVDSDEDEPMLRKTTTQIBESDVNVEGEVWKLNLHVHMGFIADNQ 668
 DB 636 LPLRPOEMEVDSDEDEPMLRKTTTQIBESDVNVEGEVWKLNLHVHMGFIADNQ 695
 QY 669 MNHACMLFVENYGOKI IKKNLCBNFMLHVSMDPFLISMSIDKAVTKLREMOQKLEK 728
 DB 696 MNHACMLFVENYGOKI IKKNLCBNFMLHVSMDPFLISMSIDKAVTKLREMOQKLEK 755
 QY 729 ESASPANBEITEBONGTANGFSEINSKERALETDSVSGVSKOKK 776
 DB 756 ESASPANBEITEBONGTANGFSEINSKERALETDSVSGVSKOKK 803

RESULT 4
 US-09-764-864-931
 ; Sequence 931, Application US/09764864
 ; Patent No. US20020132753A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT223
 ; CURRENT APPLICATION NUMBER: US/09/764,864
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1792
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 931
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-764-864-931

Query Match 50.1%; Score 2043; DB 3; Length 388;
 Best Local Similarity 99.5%; Pred. No. 1.5e-150;
 Matches 386; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 GPTLOFTLWGTETNDKSTAPIAKPLATNSSESLHQENKPGSVKPTQTAVKESLTTDQ 448
 DB 1 GPTLOFTLWGTETNDKSTAPIAKPLATNSSESLHQENKPGSVKPTQTAVKESLTTDQ 60
 QY 449 TRKEKOTPENRQKLI FYQFLYNNNTROOTEARDLHCPWCTLNCRKLYSLKHLKLGCH 508
 DB 61 TRKEKOTPENRQKLI FYQFLYNNNTROOTEARDLHCPWCTLNCRKLYSLKHLKLGCH 120
 QY 509 SRFINNYVYHPKCARIDVSNCEYDGSYAGNPODIHROPFAFSRNGPVKRTPTITILV 568
 DB 121 SRFINNYVYHPKCARIDVSNCEYDGSYAGNPODIHROPFAFSRNGPVKRTPTITILV 180
 QY 569 RPKRTKASMSSEFLSEDEGEVQRTYSOGHNLRYFHSDDCPLRPOEMEVDSDEKDP 628
 DB 181 RPKRTKASMSSEFLSEDEGEVQRTYSOGHNLRYFHSDDCPLRPOEMEVDSDEKDP 240
 QY 629 LREKTTTQIBESDVNVEGEVWKLNLHVHMGFIADNQMNHACMLFVENYGOKI IKKN 688
 DB 241 LREKTTTQIBESDVNVEGEVWKLNLHVHMGFIADNQMNHACMLFVENYGOKI IKKN 300
 QY 689 LCRNFMHLVSMHDFNLISMSIDKAVTKLREMOQKLEKESASPANBEITEBONGTANG 748

DB 301 LCRNFMHLVSMHDFNLISMSIDKAVTKLREMOQKLEKESASPANBEITEBONGTANG 360
 QY 749 FSEINSKERALETDSVSGVSKOKK 776
 DB 361 FSEINSKERALETDSVSGVSKOKK 388

RESULT 5
 US-10-942-711-54

; Sequence 54, Application US/10942711
 ; Publication No. US20050132446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Caroline
 ; APPLICANT: Gendall, Anthony
 ; TITLE OF INVENTION: Methods and means for modification of plant characteristics us1
 ; FILE REFERENCE: Mewburn
 ; CURRENT APPLICATION NUMBER: US/10/942,711
 ; PRIOR FILING DATE: 2004-09-16
 ; PRIOR APPLICATION NUMBER: US/09/890,220
 ; PRIOR FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: PCT/GB00/00248
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: GB 9901927.5
 ; PRIOR FILING DATE: 1999-01-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 54
 ; LENGTH: 367
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-942-711-54

Query Match 47.7%; Score 1944; DB 5; Length 367;
 Best Local Similarity 100.0%; Pred. No. 7.2e-143;
 Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 IAKPLATNSSESLHQENKPGSVKPTQTAVKESLTTDQTRKEKTPPENRQKLI FYQF 469
 DB 1 IAKPLATNSSESLHQENKPGSVKPTQTAVKESLTTDQTRKEKTPPENRQKLI FYQF 60
 QY 470 LYNNNTROOTEARDLHCPWCTLNCRKLYSLKHLKLGHSRPIFYVYVHPKCARIDVSN 529
 DB 61 LYNNNTROOTEARDLHCPWCTLNCRKLYSLKHLKLGHSRPIFYVYVHPKCARIDVSN 120
 QY 530 EGYDGSYAGNPODIHROPFAFSRNGPVKRTPTITILVCRPKRTASMSSEFLSEDEGEV 589
 DB 121 EGYDGSYAGNPODIHROPFAFSRNGPVKRTPTITILVCRPKRTASMSSEFLSEDEGEV 180
 QY 590 QORTYSSGHNLRYFHSDDCPLRPOEMEVDSDEDEPMLRKTTTQIBESDVNVEGEK 649
 DB 181 QORTYSSGHNLRYFHSDDCPLRPOEMEVDSDEDEPMLRKTTTQIBESDVNVEGEK 240
 QY 650 WKLNLHVHMGFIADNQMNHACMLFVENYGOKI IKKNLCBNFMLHVSMDPFLISIM 709
 DB 241 WKLNLHVHMGFIADNQMNHACMLFVENYGOKI IKKNLCBNFMLHVSMDPFLISIM 300
 QY 710 SIDKAVTKLREMOQKLEKESASPANBEITEBONGTANGFSEINSKERALETDSVSGVSK 769
 DB 301 SIDKAVTKLREMOQKLEKESASPANBEITEBONGTANGFSEINSKERALETDSVSGVSK 360
 QY 770 QSKKOKL 776
 DB 361 QSKKOKL 367

RESULT 6
 US-09-764-864-911
 ; Sequence 911, Application US/09764864
 ; Patent No. US20020132753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 911
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-911

Query Match
Best local Similarity 99.6%; Score 1497; DB 3; Length 289;
Matches 283; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 493 NCRKLSLLKHLKLCRSRIFNYVYHPKGRIDVINSINCYDGSYAGNPQDIHQPGPAVS 552
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DB 6 DCRKLSLLKHLKLCRSRIFNYVYHPKGRIDVINSINCYDGSYAGNPQDIHQPGPAVS 65
QY 553 RRGVPRPTITHLVCRPKTKASMSSEFLSEDEGEVQOQTYSSGHNRLYFHSDTCLPLR 612
;
DB 66 RRGVPRPTITHLVCRPKTKASMSSEFLSEDEGEVQOQTYSSGHNRLYFHSDTCLPLR 125
QY 613 PQMEVDSDEKDPKPEMLREKTIQIEFSPDVNCEKEMVLMNLHYMKGFIDNOMNHA 672
;
DB 126 PQMEVDSDEKDPKPEMLREKTIQIEFSPDVNCEKEMVLMNLHYMKGFIDNOMNHA 185
QY 673 CMLFVENVGQKIKKMLCRNFMHLVSMHDFNLISIMSIDKAVTKLREMOQKLEKESAS 732
;
DB 186 CMLFVENVGQKIKKMLCRNFMHLVSMHDFNLISIMSIDKAVTKLREMOQKLEKESAS 245
QY 733 PANEETEEONGTANGPSEINSEKALETDSVGSVKOSKQKQL 776
;
DB 246 PANEETEEONGTANGPSEINSEKALETDSVGSVKOSKQKQL 289

RESULT 7
US-09-764-864-1369
; Sequence 1369, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1369
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (121)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1369

Query Match
Best local Similarity 96.8%; Score 1453; DB 3; Length 292;
Matches 275; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 233 RKDVSCPIQVPTGKQKQVLIPLDNLQTKGNPPSLAVSSEFPPSSSHVVKYSLLFRYT 292
;
DB 1 KDVSCPIQVPTGKQKQVLIPLDNLQTKGNPPSLAVSSEFPPSSSHVVKYSLLFRYT 60
QY 293 RGRREPFNGMIGETENENIDVNEELPARRKRREDEKTFVQOMTVFDGNRLQLDGEY 352
;
DB 61 RGRREPFNGMIGETENENIDVNEELPARRKRREDEKTFVQOMTVFDGNRLQLDGEY 120
QY 353 EVAMQEMECPISKRATWETILDGKRLPPFTFSQPTLQFTLAWTGETNDKSTAPIAK 412
;
DB 121 XVAQMCEMCEPISKRATWETILDGKRLPPFTFSQPTLQFTLAWTGETNDKSTAPIAK 180
QY 413 PLATRNSESLHQBKNRPGSYKPTQITAVKESLTTDDQTRKEXTPNENRQKALFYQFLYN 472
;
DB 181 PLATRNSESLHQBKNRPGSYKPTQITAVKESLTTDDQTRKEXTPNENRQKALFYQFLYN 240
QY 473 NNTROQTEARDLHCPWCTLCNCKLYSLKHLKLCRSRIFNYV 516
;
DB 241 NNTROQTEARDLHCPWCTLCNCKLYSLKHLKLCRSRIFNYV 284

RESULT 8
US-11-097-143-41697
; Sequence 41697, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41697
; LENGTH: 955
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-41697

Query Match
Best local Similarity 32.9%; Score 1127.5; DB 6; Length 955;
Matches 273; Conservative 177; Mismatches 240; Indels 179; Gaps 26;

QY 65 MTDARREDSLKKKIQPLSLTLSSSVSRGNV---STPPRHSGSLTPPVTPPTTPSS 120
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```

Db      1 MAPAKKREKDS-----NPDGSANGIIGLTHGAPDASNNGSTVPTAEQVKLN 49
Qy      121 SFRSSTP-----TEPTQYRFLKRTNRLIAPFLFRLTLTYMHRSRTNKKTKRVDM 174
Db      50 GHQBOEQLFLOAFEEPTQYRFLRNHETNPIFLNRKTSYMEKERSNNKKISFQVNSM 109
Qy      175 LSKVEKMGKEBESHLSA-HLQLTFGFPHKNDKXSPNSENQ-----NSVYLE 222
Db      110 LEST-----TQKSEAVSQNYLHVITYDSLHEKLPARLDNBSGDLLOEQLLCAAGSASVYE 164
Qy      223 VLVAVCHKRRDVSCEPIRQVPTGKKQVPLIPDLNQTCKGNPPSLAVSNEPEP-SNSHM 281
Db      165 TLYVITRSKRDSTLDFQELLKSCSQIYYNP---KDRVGHATISILPQTRPMGEQIT 221
Qy      232 VKSYGLLRVYTRPGRRREFGNGTNEIMDVNEELPARKKNREDGKTFVACMTVPK 341
Db      222 L--YLLLFRIK-----VLSPSTCN--DENAEPTP-NKRSRPN-EKMFGESELILEX 266
Qy      342 NRRLQLDGEYEVAMQEMECPI---SKKRAWTETILQGRLP---PFETFSQGPLQPT 395
Db      267 SSGF-ITGEYRAMLOPLANSTISKSPKCKTWTMPD-SYPLSLITDVYQSPMLKFN 324
Qy      336 LRMGTENDKSTAPIAKPLATR-----NBSLHQEN-----KPGSVKPTQTI 437
Db      325 LTL--SNEQLPEMISAPELQRYVQHLDAVAMNMYNNNNNNNCSGLKNGSGGNGSTV 381
Qy      438 AVKESLTLDLQTRKCKDTPNENRQKRLIFYOPLYYNNTRQOETEADDLHCPECTLANCKL 497
Db      382 C-----KTPP---EHIQIYVNFMYNSNNTROQTEYQELNCPWCGJDLCLRL 423
Qy      498 YSLKHLKLCHSRFIFNTVYVHKARIDVSYNECDSYAGNODIHPGPAFSRN-GP 556
Db      424 YALLKHLKLCARFETQOPAGSGARIDVTINDAYDSYAGSPYDLAPSGSSSFRKTCGP 483
Qy      557 VKRPIITHLVCRPRRTKASMSSEFLSEBDEVEBOQRTYSGCHNRLYFHSDTCLPLRQEM 616
Db      484 VRRTSVTSLMVCRRPCKTCLDEFLDEDEISNRSYITGNRLYHHTETCLPLPHREL 543
Qy      617 EVDSDDEQPEWLEKTKTTOLEBESDVNVEGEKVCNKLNLHYMKGFADNOMNACHMLF 676
Db      544 DIDSSESDPLMLRKTKTOMTDEFSDVNEGEKELMKNLNLHYMRGFGVDCOLPLACMF 603
Qy      677 VENYGOKIIKKULCENFMHLVSMHDFNLISMSIDKAVTKLREMOQKLEKES----- 730
Db      604 LPAKTEIVRKULYNFILMCSLPDYGLIAETVYKTVQKLQGLSKYAMAGQELMQROR 663
Qy      731 -----ASPANEITE----- 740
Db      664 EEOUKYWLVDGHHKKQEDPKTLKSPQKRAPRADQASTSASSTSGSGSSSMQPKMRA 723
Qy      741 -----BONGTANGFSEINSEKALETDSVSGVSKQSKQKYL 776
Db      724 HLKRGSAASDPGVQSKGTENGNGSNS-----SSSNSKVAKKADQPL 767

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RESULT 9

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US-09-764-864-1355
; Sequence 1355, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1355
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens

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```

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (166)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1355

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```

Query Match      22.5%; Score 919; DB 3; Length 175;
Best Local Similarity 94.3%; Pred. No. 2.2e-63;
Matches 165; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy      466 FYOPLYYNNTRQOETEARDDLHCPECTLANCKLYSLKHLKLCHSRFIFNTVYVHKARID 525
Db      1 FYOPLYYNNTRQOETEARDDLHCPECTLANCKLYSLKHLKLCHSRFIFNTVYVHKARID 60
Qy      526 VSIINECTGSAAGNPQDIHRQPGAFSNGVYKTPITHIIVCRPKRTKASMSSEFLSESD 585
Db      61 VSIINECYGSAAGNPQDIHRQPGAFSNGVYKTPITHIIVCRPKRTKASMSSEFLSESD 120
Qy      586 GEVEQORTYSSGHNRLYFHSDTCLPLRQEMVDSDEKDEPMLREKTTIOIEBF 640
Db      121 GEVEQORTYSSGHNRLYFHSDTCLPLRQEMVDSDEKDEPMLREKTTIOIEBF 175

```

RESULT 10

US-09-874-162A-2

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; Sequence 2, Application US/09874162A
; Patent No. US20020155452A1
; GENERAL INFORMATION:
; APPLICANT: Koonitz, Jason
; APPLICANT: Sklar, Jeffrey
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZ2 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874,162A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-162A-2

```

```

Query Match      16.2%; Score 661; DB 3; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MTGIAAASFPSNTCRFGCGGHAPEPTLADLIEHIDNHIDMPRLVLEKQELQOPTYVALSY 60
Db      1 MTGIAAASFPSNTCRFGCGGHAPEPTLADLIEHIDNHIDMPRLVLEKQELQOPTYVALSY 60
Qy      61 INREMTDAARREOQSLKKKTIQPKLSLTSSSVSRGNVSTPRHSGSLTPVTPPTIPSS 120
Db      61 INREMTDAARREOQSLKKKTIQPKLSLTSSSVSRGNVSTPRHSGSLTPVTPPTIPSS 120
Qy      121 SFRSSTP 128
Db      121 SFRSSTP 128

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RESULT 11

```

US-10-144-198-16
; Sequence 16, Application US/10144198
; Publication No. US20030219748A1
; GENERAL INFORMATION:

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/ APPLICANT: Origene Technologies Inc
/ TITLE OF INVENTION: Regulated Prostate Cance Genes
/ FILE REFERENCE: 9U 105 R1
/ CURRENT APPLICATION NUMBER: US/10/144,198
/ CURRENT FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 16
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-144-198-16

Query Match      16.2%; Score 661; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 60
DB 1 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 60

QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
DB 61 INRFMTDAARREOESLKKKIOPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120

QY 121 SFRSSTPT 128
DB 121 SFRSSTPT 128

RESULT 12
US-10-104-047-2404
/ Sequence 2404, Application US/10104047
/ Publication No. US20030236392A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 2404
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-104-047-2404

Query Match      16.2%; Score 661; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 60
DB 1 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 60

QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
DB 61 INRFMTDAARREOESLKKKIOPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120

QY 121 SFRSSTPT 128
DB 121 SFRSSTPT 128

RESULT 13
US-09-764-864-1334
/ Sequence 1334, Application US/09764864
/ Patent No. US20020132753A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
```

```
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT223
/ CURRENT APPLICATION NUMBER: US/09/764,864
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 1792
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1334
/ LENGTH: 278
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (145)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1334

Query Match      16.0%; Score 652; DB 3; Length 278;
Best Local Similarity 99.2%; Pred. No. 2.9e-42;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 60
DB 36 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 95

QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
DB 96 INRFMTDAARREOESLKKKIOPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPPSS 155

QY 121 SFRSSTPT 128
DB 156 SFRSSTPT 163

RESULT 14
US-09-764-864-884
/ Sequence 884, Application US/09764864
/ Patent No. US20020132753A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT223
/ CURRENT APPLICATION NUMBER: US/09/764,864
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 1792
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 884
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-764-864-884

Query Match      11.7%; Score 476; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 6e-29;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 60
DB 51 MTGIAASFPSNTRCGGCGLHPTLADLIEHIEDNHIDTDPRVLEKQELQOPTVYALSY 110

QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSVSVS 93
DB 111 INRFMTDAARREOESLKKKIOPKLSLTLSVSVS 143

RESULT 15
US-10-029-386-28495
/ Sequence 28495, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
```



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; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: A60MICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28495
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR17.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P23477, EVALUE 2.70e+00
US-10-029-386-28495
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Query Match      8.8%; Score 359; DB 4; Length 69;
Best Local Similarity 98.6%; Pred. No. 2.7e-20;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 569 RPKRTKASMSSEFLSBDGSEVEOQRTYSSGHNRLYFHSDTCLPLRPOEMEVDSDEKDPW 628
DB 1 RPKRTKASMSSEFLSBDGSEVEOQRTYSSGHNRLYFHSDTCLPLRPOEMEVDSDEKDPW 60
QY 629 LREKTTITOI 637
DB 61 LREKTTITVI 69
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Job time : 172 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 13:18:27 ; Search time 28 Seconds
(without alignments)
864.464 Million cell updates/sec

Title: US-09-874-162a-8

Perfect score: 4078
Sequence: 1 MTGIAASFNTCRFGCGG.....KALETDSVSGVSKQKQKL 776

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.New:*
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2: /SID5/ptodata/1/pubppa/US06.NEW.PUB.pcp:*
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8: /SID5/ptodata/1/pubppa/US60.NEW.PUB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	661	16.2	243	7	US-11-072-512-2404 Sequence 2404, Ap
2	176.5	4.3	1142	7	US-11-087-099-3831 Sequence 3831, Ap
3	153.5	3.8	1279	6	US-10-793-626-3188 Sequence 3188, Ap
4	147	3.6	2228	6	US-10-511-096-2 Sequence 2, Appl1
5	147	3.6	2230	6	US-10-511-096-4 Sequence 4, Appl1
6	147	3.6	2250	6	US-10-511-096-6 Sequence 6, Appl1
7	147	3.6	2252	6	US-10-511-096-8 Sequence 8, Appl1
8	140.5	3.4	5406	6	US-10-995-561-774 Sequence 774, Appl1
9	139.5	3.4	1085	7	US-11-087-099-11646 Sequence 11646, A
10	138.5	3.4	2896	7	US-11-124-368A-306 Sequence 306, App
11	138.5	3.4	2896	7	US-11-124-367A-434 Sequence 434, App
12	135	3.3	3803	6	US-10-995-561-773 Sequence 773, App
13	135	3.3	3960	6	US-10-995-561-771 Sequence 771, App
14	135	3.3	5335	6	US-10-995-561-777 Sequence 777, App
15	135	3.3	5415	6	US-10-995-561-779 Sequence 779, App
16	135	3.3	5464	6	US-10-995-561-775 Sequence 775, App
17	135	3.3	5935	6	US-10-995-561-776 Sequence 776, App
18	134.5	3.3	1299	6	US-10-204-639-70 Sequence 70, Appl
19	131.5	3.2	4384	6	US-10-821-234-1120 Sequence 1120, Ap
20	131	3.2	2426	7	US-11-203-806A-11 Sequence 11, Appl
21	128.5	3.2	2910	6	US-10-330-773-39 Sequence 39, Appl
22	128.5	3.2	3256	7	US-11-124-368A-304 Sequence 304, App
23	128.5	3.2	3256	7	US-11-124-367A-432 Sequence 432, Appl
24	128	3.1	798	6	US-10-514-531-2 Sequence 2, Appl1
25	124.5	3.1	1347	7	US-11-087-099-5370 Sequence 5370, Ap

26	122.5	3.0	1160	7	US-11-087-099-6576 Sequence 6576, Ap
27	122.5	3.0	2668	7	US-11-124-368A-215 Sequence 215, App
28	122	3.0	1033	7	US-11-087-099-8833 Sequence 8833, Ap
29	121	3.0	2251	7	US-11-183-203-30 Sequence 30, Appl
30	121	3.0	2351	7	US-11-244-087-3 Sequence 3, Appl1
31	121	3.0	2351	7	US-11-267-631-49 Sequence 49, Appl
32	120	2.9	943	6	US-10-475-204-34 Sequence 34, Appl
33	119.5	2.9	599	6	US-10-995-561-812 Sequence 812, Appl
34	119.5	2.9	2897	6	US-10-499-715-2 Sequence 2, Appl1
35	119.5	2.9	8746	7	US-11-098-686-10232 Sequence 10232, A
36	119	2.9	760	7	US-11-087-099-1634 Sequence 1634, App
37	119	2.9	1346	7	US-11-060-005-2 Sequence 2, Appl1
38	119	2.9	1609	7	US-11-087-099-4181 Sequence 4181, App
39	118	2.9	463	7	US-11-096-568A-1230 Sequence 1230, App
40	118	2.9	464	7	US-11-096-568A-1229 Sequence 1229, App
41	118	2.9	480	7	US-11-096-568A-1228 Sequence 1228, App
42	118	2.9	915	7	US-11-087-099-6117 Sequence 6117, App
43	118	2.9	1037	7	US-11-087-099-6333 Sequence 6333, App
44	117	2.9	2096	6	US-10-995-561-606 Sequence 606, App
45	117	2.9	2351	6	US-10-995-561-608 Sequence 608, App

ALIGNMENTS

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RESULT 1
US-11-072-512-2404
; Sequence 2404, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2404
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-2404

Query Match      16.2%; Score 661; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTGIAASFNTCRFGCGGHPPLADLIEHIDNHTDPRVLEKQELQOPTVVALSY 60
DB      1 MTGIAASFNTCRFGCGGHPPLADLIEHIDNHTDPRVLEKQELQOPTVVALSY 60
QY      61 INRFMTDAARREOSLKKKIQPKLSLTLSVSRGNVSTPPRHSSGSLTPPTPTPSS 120
```

```

Db      61  INFMFMDAAREBESLKKKIOPKLSLTLSSVSGNVSTPRRSGSLTPVTPITPSS 120
Qy      121  SFRSSTPT 128
Db      121  SFRSSTPT 128

```

RESULT 2

```

US-11-087-099-3831
; Sequence 3831, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3831
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-087-099-3831

```

Query Match 4.3%; Score 176.5; DB 7; Length 1142;

Best Local Similarity 20.8%; Pred. No. 5.4e-05; Indels 213; Gaps 35;

Matches 152; Conservative 102; Mismatches 264;

```

Qy      41  DPRVLEKQELQDP-----TYVALSYINRPMFMDAAREBESLKKKIOPKLSLTLSS-SVS 93
Db      337  DEPGI-KERKREPGANAKETLVALLY--RFKCDT---QKELIKQGVKKRQSSISVS 389
Qy      94  RG-NVSTPP-----RHSSGSLTPPVTPPI-----TPSSFRSSTPTPTQIYRFLKTR 140
Db      390  PSKVVSTTPQRRNRRESLISVTSRKRPISFNKFTASASSSNLTPGSSKRLSKNFSK 449
Qy      141  NLAPFIAFIAHRTLYVSHRNRTNI--KRTEKVDMDLSTVEKMKGEOS-----187
Db      450  KKLSTIVNOSPPRPAS-RNGASVIVNEKQKQASISTTKKQKRSRSIKRMSLIPSMK 508
Qy      188  HSLSAHLQLTFTGFPHKNDKPPNSSEONSVTLVLVAVK-----CHKRKDVSC 238
Db      509  RESVTTLMSTVAKLAEDDDMEYIEKETKRTSSNFATLIDEIFEYKEQIRKEKELE 568
Qy      239  PIQVPPVG-----KQVPL-IPDLNQ-----258
Db      569  KYREARARELEERRRQKEKERARKLLEKEDLKRQKEELKQIIEIDISLBQELSKHKE 628
Qy      259  -TKGNPPLAVSNEFEPNSHVKYSLLFR-----VTRPGRRPFGNMGINGETNENI 311
Db      629  EKLDGNIRISAMWENEEKINHLVDIDNILRRNSLQTRPVSRIDPGIMSSPTEEV 688
Qy      312  DVNEELPARRKRRRDEKTFVQW-----TVFDKRRRLQDLDEYE--VAMQEN-EE 361
Db      689  SPVE--PKRTYENRELTEKKILETIRSKFAGSSFNIDKELKSKVEYPIIAPQRSE 746
Qy      362  CPTSKKRAWTETLI--DGKLLPPE--TFSQPTLOFTIRWGETNDKSTAPLAKLAT 416
Db      747  RVVSDSNDGYESLILPDGNGVSQDKSTATTAPVSDGRLKISE-----IRVQFT 798
Qy      417  RNSESLHQENKPGSVKPTQTLAVGESLTTDLQTRKEKDTPENRQKRIFYQFLVNNTR 476
Db      799  RKRHRHSESNNKRLSV--LSWYSTESFTNLDILKGNLDVNNQOSRI-----845
Qy      477  QQTEARDLHCPWCTLNCRLYSLLKHLKLGHSRFFINYYVHPKGAIRDVINECYDGSY 536
Db      846  PTPRSADD-----SEFLFE-----TVAE--EAEY 867
Qy      537  AGNPQDIHR-----QGFPA--PSRNGVKTPTPTTHILVCRPKTKASMS 579
Db      868  TGNSSNDERLYDVGDSTIKDKSALKNFADRFGNSNEAKOTDNLHLPLPLNGDNLRLK 927

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```

Qy      580  FLESEDEVEOQRTYS-----SGHNRLYFHSIDTCLPLRPOEMVSEDEKDPEN-----628
Db      928  -QNSQEGDQAHKPKISMIPESGSS--HTE-----KEFNNEKEKEKKPEQHKEQ 976
Qy      629  -LREKTTIQIE 638
Db      977  EKREKVVDDME 987

```

RESULT 3

```

US-10-793-626-3188
; Sequence 3188, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3188
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3188

```

Query Match 3.8%; Score 153.5; DB 6; Length 1279;

Best Local Similarity 17.5%; Pred. No. 0.0034; Indels 211; Gaps 35;

Matches 141; Conservative 146; Mismatches 310;

```

Qy      30  IEHIEDNHIDTPRVLEKQELQDPYVALSYINRPMFMDAAREBESLKKKIOPKLSLTLSS 89
Db      528  LEKINNIOPTQTKNAQKQINDKAQEOILQINN--TPDATBEKQATNRVNGAQAID 586
Qy      90  SSVSGNVSTPPRHSSGSLTPPVTPPTPTPSSFRSSTPTPEPTQIYRFLTRNIAIFLH 149
Db      587  -----NINN--AHSQEVNESKTSIATIKSVQPVNIKPPAINGSLTQEAN-----630
Qy      150  RLLTYVSHNSRNIRK-----TFKVDMLSKVEKMGEOBSHLSAH---LQLTFT 199
Db      631  NQKTLIGDNQATDDEKAKQULVTKLNEQLOKIHESQDQNVQVNAQAATAIKLI-- 688
Qy      200  GFPHKNDKPSNSENEQNSVTLVLVAVKCHKRKDVSCPIRQVPTGKKQVPLIPDLNQT 259
Db      689  -----NANAHKQDAIN--ILTNLAESKSDIRA--NQDATTEKNTAIGSIDPT 734
Qy      260  KPGNPSLAVSNEFEPNSHVKYSLLFRVTRPGRREPNGING-----305
Db      735  -----LAQARNNINGANTNALVDENL-----EDKQKQIQRVLSVSTQTKYQAKADIQA 782
Qy      306  -----ETNENIDVNEELPARRKRRR-----DEKTFVQWTVFD-KNRLQLDLGE 351
Db      783  IGOQRSTIDQNOATTEBEKQKALERNQETNGVNDIQAALANQVTEKNNILETIRNV 842
Qy      352  YEVAQWEMEBECPISKRAWTETLIDGKRLPPPTFSQPTL---QTLRWGTENDKSTA 408
Db      843  EPIVIVKPRANEILIRKKAQEQTLINQ-----NQDATLEBKQALGLGEVKQKALN 894
Qy      409  PIKPLATRNSESLSHOEN---KPGSVKPTQTLA--VKSLLTDLQTRKEKDTPENRQK 462
Db      895  QVSO--AHSNNNDVIKENNGIAKISEVHPEITIKRKAQEIQEDQAS--QIDTINAN---947
Qy      463  LRIFYQFLVNNNRQQTTEARDLHCPWCTLNCRLYSLLKHLKLGHSRFFINYYVHPKGA 522
Db      948  -----NKSNEEKSAAID-----RVNAKIDAI-----NNTTAAATTT 979
Qy      523  RIDVINECYDGSYAGNPQDIHRQPGFAFSRNGPVKRTPTTHILVCRPKTKASMSBEFL 582

```

Db 980 QV---VN---DAKNSNTSISOILPSTA-----VK-----TNALALAEAKNAIIOQ 1023
QY 583 SEDGEVOOQRTYSSGHNRYFHSPTCLPLRPOEMEVDSDEKDPKREKTIQI----- 637
Db 1024 TNATATREKSEKANKVDR-----OEBADANTLKATHTDEVNINIKN 1064
QY 638 BEFSDVNEGEKEVMKLMNLHVAKHGFIADONMNAHMLFVENYGOKIIR----- 686
Db 1065 QAVONINAVQVEVIKQN-----AKQOLNQ-----PIDNQ-KKIENTDPAITLEKA 1110
QY 687 --KNCRNPMHL---VSNHDPNLLSINSIDAVTKLRMOOKLEKESASPAHEETEE 741
Db 1111 EANRLQONVLTSTSEIANVDHNEVDQALDKARPKIEAIVPOVSKGRDALNAIOEAFNS 1170
QY 742 QNGTANGFSEINSKEKALETDSVGSVK 769
Db 1171 QT-----OEIOEKOEATNEBKTEALNK 1192

RESULT 4
US-10-511-096-2

Sequence 2, Application US/10511096
Publication No. US20060052280A1
GENERAL INFORMATION:
APPLICANT: Evotec Neurosciences GmbH
TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
FILE REFERENCE: P67813US1
CURRENT APPLICATION NUMBER: US/10/511,096
CURRENT FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 2228
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-096-2

Query Match 3.6%; Score 147; DB 6; Length 2228;
Best Local Similarity 18.2%; Pred. No. 0.023;
Matches 152; Conservative 148; Mismatches 308; Indels 228; Gaps 36;

QY 30 IEHEDNHIDDPVLEK-----OEIOQPTVALSYINRFMTDAARBOESLKKKIQ 81
Db 330 LEKIDLMMAEKTKILITQLDAKNLIEQLEQDKGVIAETRKQMETLEMKEBEITAQLRS 389
QY 82 PKLSLTSSSVSRGNVSTPRHSSGSLPPVTPPTTPSSSPRSSPTPEPTQIYRFLKRN 141
Db 390 RIKQMTTQGEELREQEKESERAAFELEKALSTAQKTEBARKKLAEMDEQIKTIEKTS 449
QY 142 LIAPFLHRTLTVMHRSRTNIRKTFV-----DMLSKVEKA-----KGBOESHSL 190
Db 450 -----BEHISLQOELSRVQEVVDVWKKSSBEOIATLQKLEHKEKLARKBOE---L 496
QY 191 SAHLQLTGTFPHKNDKPSNSENEONSVTLEVL---LVKVCCHKRKOVSCPIROVPYK 247
Db 497 TKKLTQTRERF-----OEOMKVALKSSQSEYIKLSOEKBOESLALBELBLQK 544
QY 248 KQV-----PLPDLNQTRKGNFPPLAVSSNEPEPSNSHNVKSYSLFVTRPGRREFNGM 302
Db 545 KAILTESENKLRDLOQ-----BAETVTRTILLESLSLEKSLQENKQNSDL 590
QY 303 ---INGETNENIDVNEELPARKKRNREDEKTFVAQMTVPDKNRRLQLLDGEYEVAMQEM 359
Db 591 AVHLEAEKNKH---NKEITVAVBKHTLESLKHQODALM---TEKLOVYLKQOYQTEMEKL 645
QY 360 -ECPISKRAWTETILDOCKRLPPETFSQGPFLQFTLRWGETNDKSNAP-----AK 412
Db 646 REKGEQK-----ETLLDKKEI-IFQAHIE-----ENNEKTELEKIDVQTELE 687
QY 413 PLATNNSSL---HOENKRGVYKPTQTITAVKSLTTLDTQTRKEXDTPENNRQKLAIFYQF 469

Db 688 SLSSSELSEVLKARHKLBEELSVLKDQTDKMOELEAKNDEOK-----NHHQOQVDSIIE 742
QY 470 LYNNNTROQTEARDLDHCPCWCTLNCRKLYSLI-----KHKLCHSRFIRNYVYHPRGARID 525
Db 743 HEVSTORTKALKDQIN-----QLELLKERDKHLK-----EHOAHVENLEAD 785
QY 526 VSINECYGSGVYAGNQDIIHQGFAPFASRNGPVKRTPIHILVCRPKRTYASSEF----- 580
Db 786 IKRSE-GELQQAASALDVFGYSQSA-----TH-----EQRTAYEEQALQLOQ 826
QY 581 ---LESED-----GEVBOQRTYSSGHNRYFHSPTCLPLRPOEMEVDS-----EDEK 624
Db 827 KLIDLETERILITTKQAVVEAOK-----KDVCTELDAHKIQVODLMQOLEKON 874
QY 625 DEWIREKTIQIEFSDVNEGEKEVMKLMNLHVAKHGFIADONMNAHMLFVENYGOKI 684
Db 875 SEMEOKVSILTQVVE-SKLEBDENKQBOETKQILVEKENNITL--QNRBOGKEIEITQKL 931
QY 685 IKONLCRNPMHLVSMHDPNLLSINSIDAVTKLRMOOKLEKESASPAHEE----- 737
Db 932 SAKE-----DSIHILN-----BEYETKFNQEKREKAKVQKAKEMQETLKKLL 975
QY 738 -----ITBEONGTANGFSEINSKEKAL-----TDSVSGVSKQSKQ 774
Db 976 DQEALEKKELENTA---LELSQEKQFNAKMLEMAQANSAGISDAVSRLETNQEKQ 1028

RESULT 5
US-10-511-096-4

Sequence 4, Application US/10511096
Publication No. US20060052280A1
GENERAL INFORMATION:
APPLICANT: Evotec Neurosciences GmbH
TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
FILE REFERENCE: P67813US1
CURRENT APPLICATION NUMBER: US/10/511,096
CURRENT FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 2230
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-096-4

Query Match 3.6%; Score 147; DB 6; Length 2230;
Best Local Similarity 18.2%; Pred. No. 0.023;
Matches 152; Conservative 148; Mismatches 308; Indels 228; Gaps 36;

QY 30 IEHEDNHIDDPVLEK-----OELOQPTVALSYINRFMTDAARBOESLKKKIQ 81
Db 330 LEKIDLMMAEKTKILITQLDAKNLIEQLEQDKGVIAETRKQMETLEMKEBEITAQLRS 389
QY 82 PKLSLTSSSVSRGNVSTPRHSSGSLPPVTPPTTPSSSPRSSPTPEPTQIYRFLKRN 141
Db 390 RIKQMTTQGEELREQEKESERAAFELEKALSTAQKTEBARKKLAEMDEQIKTIEKTS 449
QY 142 LIAPFLHRTLTVMHRSRTNIRKTFV-----DMLSKVEKA-----KGBOESHSL 190
Db 450 -----BEHISLQOELSRVQEVVDVWKKSSBEOIATLQKLEHKEKLARKBOE---L 496
QY 191 SAHLQLTGTFPHKNDKPSNSENEONSVTLEVL---LVKVCCHKRKOVSCPIROVPYK 247
Db 497 TKKLTQTRERF-----OEOMKVALKSSQSEYIKLSOEKBOESLALBELBLQK 544
QY 248 KQV-----PLPDLNQTRKGNFPPLAVSSNEPEPSNSHNVKSYSLFVTRPGRREFNGM 302
Db 545 KAILTESENKLRDLOQ-----BAETVTRTILLESLSLEKSLQENKQNSDL 590
QY 303 ---INGETNENIDVNEELPARKKRNREDEKTFVAQMTVPDKNRRLQLLDGEYEVAMQEM 359
Db 591 AVHLEAEKNKH---NKEITVAVBKHTLESLKHQODALM---TEKLOVYLKQOYQTEMEKL 645

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QY -----BECISKRBAWETI1DCKRLBPREFPQOGPLOTQTLAMWGETNDKSTAPI-----AK 412
Db -----REKCOEK-----ETLKKCKEI-IPAHIE-----BANEETLEKLVKQTELE 687
QY -----PLATENSESL---HOENKPKSVKPTOTIAVKSLSLTDTQTRKEKOTPNENROKRLIFYOF 469
Db -----SLSSELSBVLKARHKLEBLSVLKODTDMMKQELBAMDBOK-----NHHQOQVDSIIE 742
QY -----LYNNNTROQTEARDLHCWCWCLNCKLYSL---KHLKLSRTEFMYVHPKCARID 525
Db -----743 HEVLSIORTKALKDOIN-----QLELLTKERDKHLK-----BEOAVENILEAD 785
QY -----526 VINEINCYDGSVANGPODRIROPGFAFSRNGPVKRTPI1HLVCRPKRTKASMEF-----580
Db -----766 IGRSE-GEHQASAKLIDVQSYOSA-----TH-----EGTRAYEBQALQLOQ 826
QY -----581 ---LESED-----GEVBOORTYSSGHNRLYFHSDTCLPLRPOEMEYDS-----EDEK 624
Db -----827 KLIDLETERILLTKQVAEVEAOK-----KDVCTELDAHKIQVODLMOOLEKON 874
QY -----625 DEWMLREKITTOLIEESPDNBEKGEVWKMLNHLVMHGFLADONMHACMLPVENYGOKI 684
Db -----875 SEMEQVSVSLTOYE-SKLEDGKKEBOQTKOILVERKENML-OMEBQCKEJ1EILTOKL 911
QY -----685 IKKNLCRNFMHLVSNMDFNLISIMSIDAVTCLREMOQKLEKGESASPANIE-----737
Db -----932 SAKK-----DSIHILN-----BEYETKFKQOEKMEKVOKAKEMQETLKKLL 975
QY -----738 -----ITRONGTANFSRINSKEKLE-----TDSVSGVSKOKKO 774
Db -----976 DOBAKTKIKRELENTA---LELSQCKEOPNAKMETMAOANSAGISDAVSRLETKNOQ 1028

```

```

RESULT 6
US-10-511-096-6
; Sequence 6, Application US/10511096
; Publication No. US20060052280A1
; GENERAL INFORMATION:
; APPLICANT: Evotec Neuroscience GmbH
; TITLE OF INVENTION: Diagnostic use of a Golgi protein for
; TITLE OF INVENTION: neurodegenerative diseases
; FILE REFERENCE: P67813US1
; CURRENT APPLICATION NUMBER: US/10/511,096
; CURRENT FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-096-6

```

Query Match 3.6%; Score 147; DB 6; Length 2250;
Best Local Similarity 18.2%; Pred. No. 0.023;
Matches 152; Conservative 146; Mismatches 308; Indels 228; Gaps 36;

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0Y 30 EHEIDNHIDUDPRYLEK-----OELOOPTYVALSYINRPMIDARROESJAKKIQ 81
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 LEKIKOLHMAEKTUKITODRDAKNLIEQOEODKGVAVIETKROHMETLEKEEELAOJRS 411
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 82 PKLSITLSSVSRCGVNSTPRPHSSGLTPPVPTPIPPSSFPSSPTPEPTIOYPLATRN 141
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 412 RIKOMTTOGEELREQEKESERAPFELBEALSTACTEARKKLKAEMDEQIKTIEKSE 471
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 142 LIAPFLHRTLYTMSHRNSRTNIKEKTEFY----DMLSKVEKM-----KGOESHSL 190
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 472 -----BEERISLOOELSRVKEOVVDVMKSSSEEOIAKLOKHEKELARKEOE---L 518
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 121 SAHLOLTGTGFPHKNDKPSNENONSUTLEVL---LYUKCHKKRKOVSPCIRIOPYPRK 247
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 519 TKKQITREBERF-----QOMYKALKEKSOSEYIKTSOEKGOESLALREJLOK 566
    | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 248 QOV-----PLPDLNOTRGNFPLSLAVSNEEFPNSHHVKSYSLLFRTRPERBERENG 302
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 567 KAILTESNNKRLQO-----BAETRTLRLEBSSLEKSLQENKOSKDL 612
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 303 ---INGETNENIDVNEELPARRKRNREDOGEKTFVAMQTFEDKNRRLQOLDGEYVMOEM 359
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 613 AVHLEAKNKH---NKEITVMWEKKTELESJLKHQODALM--TEKQVVKQOQTMEKX 667
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 360 -EECPISKRAWTETILDGKRLPRPETSOGFTLOFTLRMTGETNDKSTAPI-----AK 412
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 668 REKCEQK-----ETLLKDKET-IFOAHIE-----EMNEKTEKLDVKQTELE 709
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 413 PLATONSSL--HOENKPGSVKPYOTJAVESLTTDQTRREKOTPNENROKRLRFYOF 469
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 710 SLJSELSYLKARHKEELSYLKDQOTBMKQELAKMEOK---NNHQOVSIIKE 764
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 470 LYNNTROOTEARDDLHCPCWTLNCRKLYSL---KHLKLGSRPIFNVVYPCARID 525
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 765 HEVSIQRTTEKALKDOIN-----QLELLKERDKHLK-----EHQAHVEYLED 807
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 526 VSINECYDGSYVGNFODIHROPGFAPSRNGPVKTRPTIHLVCRPKRTASNSEF-----580
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 808 IKRSE-GELQOQSAKLVDVQSYQSA-----TH-----EOTRAYEBQLAQLOQ 848
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 581 ----LESED-----GEYEOQRTYSSGHNRLYFHSPTCLPRPQMEYDS-----EDEK 624
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 849 KLLDLETERILLTKQVAEVEACK-----KDVTELDANHKIQVDLMQOLEKON 896
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 625 DPEWLREKTIITIEEFSVDNEGEKEMKMLNHLVMWKGFIADNONMHACMLFVENVGOKI 684
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 897 SEMEQKVSILTYVE-SKLEDNKQOEQKQOLIVKEMNL--QMEGQKKEIILITQKL 953
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 685 IKKNLCRNFMHLVSMHDPNLLISMSIDKAVTLKREMOOKLEKESASAPNEE-----737
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 954 SAKK-----DSIHILN-----BEYETFKNQOEKMEKVKQAKAMEQETLKKLL 997
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 738 -----ITEKQNTANGFSEINSKEKALE-----TDSVGSVSKOSKQ 774
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 998 DOEAKTKELENTA---LELSQKEQOFNAKMLBMAQANSAGISDAVSRLETNQEQ 1050
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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```

RESULT 7
US-10-511-096-8
; Sequence 8, Application US/10511096
; Publication No. US2006005280A1
; GENERAL INFORMATION:
; APPLICANT: Evotec NeuroSciences GmbH
; TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
; TITLE OF INVENTION: neurodegenerative diseases
; FILE REFERENCE: P67813US1
; CURRENT APPLICATION NUMBER: US/10/511,096
; CURRENT FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;
; LENGTH: 2252
;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-096-8

```

Query Match	3.6%	Score 147;	DB 6;	Length 2252;
Best Local Similarity	18.2%;	Pred. No. 0.023;		
Matches 157;	Conservative 148;	Mismatches 308;	Indels 228;	Gaps 36

[illegible]

Db 472 -----EERISLOELSRVKEVDMKSSSEEOIAXIQLKHEKELAREOE---L 518
Qy 191 SAHLQUTFGFPHKNDKSPNSENEQNSVTLLEV---LVKVGCHKRKDVSCPIRQVPTCK 247
Db 519 TKKLTQTREREF-----OQOMKALERSQSEYKISOEKEQOESLALBELLOK 566
Qy 248 KOV-----PLIDLNQTKPGNFPPLAVSSENEFSPNSHWKSVSLFRTRPGRRBNFM 302
Db 567 KALPSESEKCLADLOQ-----EAEYTRTRILELESSLEKLOENKQOSKUL 612
Qy 303 ---INGETNENIDVNEELPARRKRNREDEKTFVAMTVFDKRRRLQLLDGEYEVAMQEM 359
Db 613 AVHLBAEKKH---KNEITVMVEKHKTELESLEKQODALM--TEKLOVUKQOQYTEMEL 667
Qy 360 -EECISIKKRAWTETLDOCKLPPPETFSQGTLOQTLAMGETNDKSTAPL-----AK 412
Db 668 REKCEOEK-----ETLLKDKEL-IFQAHLE-----EMNEKTEKLDVQKOTELE 709
Qy 413 PLATNNSBSL---HOENKPGSVKPTQTLAVKESLTTDLQTRKCKDTPNENROKRLRIFYOF 469
Db 710 SLSSLESEVLKARHKLBEELSVLKQOTDMKQELAKMDEOK-----NHQOQVDSIIEK 764
Qy 470 LYNNNTROQTEARDLHCPWCTLNCRKLYSLI---KHLKCHSRPIFNYYVHPKGARID 525
Db 765 HEVSIORTKALKDOIN-----OLELLKERDKHLK-----EHQAHVENTLEAD 807
Qy 526 VSINCYDGSVAGNODIHRQGFAPSRNGPVRKRPITHILVCRPKRTASNSER----- 580
Db 808 IKRSE-GELOQASAKLDVFOSYOSA-----TH-----EQTAAYEBOLAQLOQ 848
Qy 581 ----LESED-----GEVEOQRTYSSGHNRLYFHSDTCLPLRPOBMEVDS-----EDKE 624
Db 849 KLDDLETRILITKQAVAEVAK-----KDVCTELDAKTIQVQDLMQOLEKON 896
Qy 625 DPEWLEKETTIOIEEFSVDNEGEKEVMKLMNLVNHKGFIADNQNAMHACMLFVENYGOKI 684
Db 897 SEMEOKVKSLTQVYE-SKLEEDNKEOEQTKQILVEKENMIL--QMBEGQKKEIETILOKL 953
Qy 665 IKONLCRPMHLVSMHDPNLISIMSDKAVTKLAREMOCKLEKGSASANE----- 737
Db 954 SAKK-----DSIHILN-----BEYETKFKNOEKRMKVKOKAKEMOETLKKL 997
Qy 738 -----ITEONGTANGFSEINSKEKALE-----TDSVSGVSKOSKQ 774
Db 998 DOEALCKELENTA---LELSQEKQFNAKMLMAQANSAGISDAVSRLETQKQ 1050

RESULT 8
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-774

Query Match 3.4%; Score 140.5; DB 6; Length 5406;
Best Local Similarity 18.5%; Pred No. 0.24; Indels 277; Gaps 37;
Matches 172; Conservative 133; Mismatches 350;
Qy 30 IEHEDNHIDTDPRVLEKQ-----E 49

Db 1955 VEKLSIDTVASDPGVLOEOLATTKQLOEELAEHQVVEKLOKVARDIMEIEGEPARDRH 2014
Qy 50 LOQPTVVALSYINRMTPDAARE-----QESLKKKTOP-----KSL 86
Db 2015 VQETLDSILSHQOSLSYSLAESLLOKAIMQOSQOSVLSIGREVNOLBGKQVS 2074
Qy 87 TLSSSVSGONVTEPPRHSGSLTPVPTPTPTSSFSRSTPTPEPO---LYRFLATRNLA 144
Db 2075 SLSSGVIOBALATNKK-----LKQDIARQKSLAEATREMTVTRMETADSTT 2120
Qy 145 PIFLHRTLLYMSHRNSRTNKRKTFKVDMLSKV-----EKMG-----EOSHSLIS 191
Db 2121 AAVLOKGLABVSQREQLCLOQO---EKSSSLKLLPQAMFPHLSGKLOQFNNNSRMLA 2178
Qy 192 AHLQ---LFTFGFPHKNDKSPNSENEQNSV-TLEV----- 224
Db 2179 SGNDPDDITHEFOQIOELNLEMEQOENLDTLEHLVTELSGCFALDLCQHODRVONIR 2238
Qy 225 -----LVKVGCHKGRDVSCEPIRQVPTGKQVPLIDLNQTKRGNP---SLAVSNEFERS 277
Db 2239 KDFTELQTVKEREKQDASSCOEQLDEFRKLVTRFOKMLKTEBGSIPPTETMSAVBLEKQ 2298
Qy 278 NSHWKSVSYSLFRVTRPGR---REFNGMNGETNENIDVNEELPARRKRNREDEKTFVAAQ 335
Db 2299 IEHL---KSLDDMASKGTIVBEIN--CKGTSLEMLIN--EITAPDSQKTDLTE---IQ 2348
Qy 336 MTFVPKRRLQLLDG-----EYEVAMQEBECISIKKRAWTETLDOCKL--LPPPETE 386
Db 2349 CDMSVNKLKYEKLGCVLHERQESLOALINRMBE--VHKRAVSVLOMLESKEVEKLSMDAM 2406
Qy 387 SOGPTLOPTLMTGETNDKSTAPIAKPLATNNSBSLHOENKPGSVKPTQTLAVKESLTTD 446
Db 2407 S-SPTKTETVKAQASNAFLAEL-----BONSFKOK-----VKEALAGL 2446
Qy 447 LOTREKEDTPN---ENROKRLIFYOFLYNNNT-----ROQTEARDLHNC----- 487
Db 2447 LVT-----YPRNSQAEKNKKIQBELNSMRBATEVTVARQOLEBSASHLACFOAAESQL 2501
Qy 488 -PWC-----TLNCRKLYSLKHLKLCCHSRPIFNYYVHPKGARIDVSI 528
Db 2502 RPWMEKELMAGVLGPLSIDPNNLNAOK-----QOVCPMLKFEFARRQOHEO-----L 2549
Qy 529 NECYDGSVAGNODIHRQGFAPSRNGPVRKRPITHILVCRPKRKASMSERLSEDEBV 588
Db 2550 NEAAOGILITG-----PGVUSLSTQVQKE-----LOSINOQWVELTDLNRSSEOI 2595
Qy 589 EQORTYSSGHNRLYFHSDTCLPLRPOBMEVSEDEKDEPMLREKTTIOIEEFSVDNEGEK 648
Db 2596 DOALVKSQYOELLQDLSEKVRAGQRLSVQSAISTOPEAVAKQ-----OLEETSEIRSDLE 2651
Qy 649 EVMKLMNLVNHKGFIADNQNAMHACMLFVENYGOKTIKONLCRPMHLVSMHDPNLISI 708
Db 2652 QLD-----HEVKE---AQTLCDLESLVIGEOYLDELCKRL-ETVALPLQGLJDLAADR 2702
Qy 709 MSIDKAVTKLAREMO-----KLEKGSASPAHEITEBONG 744
Db 2703 NRELQALASTQOFQOMDELTFTWIDKQSOQARNCPISAKLERLOQSLOQENEBEFQKSLNQ 2762
Qy 745 TANGFSEINSKEKALETDSVSGVSKOSKQKL 776
Db 2763 HSGYEVIVVAGESLILSVPPGEBKRTIQNDL 2794

RESULT 9
US-11-087-099-11646
; Sequence 11646, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; SEQ ID NO 11646
 ; LENGTH: 1085
 ; TYPE: PRT
 ; ORGANISM: Schizosaccharomyces pombe
 US-11-087-099-11646

Query Match 3.4%; Score 139.5; DB 7; Length 1085;
 Best Local Similarity 20.1%; Pred. No. 0.03;
 Matches 121; Conservative 90; Mismatches 239; Indels 153; Gaps 28;

QY 209 SPENSEONSVTLV-LVLYVCHKKKDVSCPIROVFGKQVPLIPDLNQTGKGFPSL 267
 DB 162 SPNS--VQNNMNLNTVALGSSSTSSKK- - - - - KKKKANSASL 200
 QY 268 AV-SSEFEPSNHWKYSLLFRVT-RPGK--REFNGM-NGETNENIDVNEELPARRK 322
 DB 201 NVDDODDFE-----QVSTDAITYRNGQALSYNGSVROASMNNNNNKSKDIWS 253
 QY 323 RNREDEKTFVAQMTVADKRRRLQILDGEYEVAMQEME- - - - - CPI-SKKRATWETI 374
 DB 254 SNTREKQIREFWLSSEERR-SLVKVEKAVLQKKEQOKYSCSCVGRKRLAIEER 312
 QY 375 LDGKRLPPETFSQGPFLQFTLRWTGETN- - - - - DKSTAPIAK- - - - - PLATNSE 420
 DB 313 LEVLVAYVYELQYANICQNLANTESVNASDSGDSQKGIISDSPKLSTPLNNVPSK 372
 QY 421 SLHOENKPGSVKPTQTITAVESL-TTDLQTRKEKOTPNENRQKRLRYQPLVNNTRQOT 479
 DB 373 SLNDITDDELNSNMDVDDEVLETSL- - - - - EKNDVNO- - - - - EFVTSISNGNOT 420
 QY 480 EARDDLHCPWCTLNCRKLYSLKMLKLCCHSRPIFNYYHKGARIDVINECYDGSYAGN 539
 DB 421 -LEDTSHSPOTOPPPQPYPSKADKNSYHSDLYNF- - - - - GSSLTVK- - - - - GGLTV 468
 QY 540 PODIHRQPGFAPFASRNGPVKRTPIYTHLVCRPKTKASMEFLSEDEVEQORTYSSGN 599
 DB 469 ADDLKNNDG- - - - - KKFIEHMEGLABRRMQREDNSN 499
 QY 600 RLYPHSDTCLPLAPQEMVDSDEKDEPMLEKTIIOIEFSDVNEGEKVMKMLHVM 659
 DB 500 ---FHEP- - - - - ELYESGLEDEDEDEDE- - - - - DVDBEDLDM- - - - - 531
 QY 660 KHGFIDNQNHACMLPEVNYGOKIKKNCIRNFMHLVSMHDPNLSIM- - - - - SIDK 713
 DB 532 - - - - - TDEQMEGRFRFQIIPARLFQGRVLQAVREYVAQORQAKLLEIEENKRRQER 566
 QY 714 AVTKLRMOQKLEKGSASPANEETEEQNGTANGFSEINSKEKALETDSVGSVSKQSK 773
 DB 587 ELKIRREKRRKKQKQKLAKKE- - - - - BRORREABRLAE-QAQKALEAKRQOEARKKRE 643
 QY 774 OKL 776
 DB 644 ORL 646
 RESULT 10
 US-11-124-368A-306
 ; Sequence 306, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; FILE REFERENCE: C1001524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936

; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 21112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 306
 ; LENGTH: 2896
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-124-368A-306

Query Match 3.4%; Score 138.5; DB 7; Length 2896;
 Best Local Similarity 18.1%; Pred. No. 0.14;
 Matches 149; Conservative 113; Mismatches 285; Indels 277; Gaps 35;

QY 12 NTCRFG--GCCGHPETLADLIEH- - - - - IEDNHIDDPVLEKQELQOPTVAL 58
 DB 25 STCLFGRGIECDIRIGLPVNSKQHCIEIHQEBALHNFSNTPTQVNSVIDEPVRLKH 84
 QY 59 SYINRPMTDARBOESLK- - - - - KKIQPKSLTSSSVSGNVSTPPRH- - - - - 104
 DB 85 GDVITTIIDSPRYENSLQSGRKSTFPKIREQ- - - - - BPARRVSRSSFSDDPESDGIPL 141
 QY 105 - - - - - GGLTPPV- - - - - TPPTPSSFRSSPTPEPTQIYRFLRTRNLIAPIFLHRTL 153
 DB 142 KRRVSGGHLRPELFDENLPPVTPDK- - - - - RGEAPV- - - - - 174
 QY 154 YMSHRNSRTNIRKT--FKVDDMLSKVEKMK- - - - - GEQESHLSAHLQLTFTGFPHKNDK 207
 DB 175 - - - - - XKSLVMTHTPVYLKIIKEQPPSGKQBSGS-ELHVEVKAQSLVSPRA 222
 QY 208 SPENSEONSVTLVLLVAVKCHKKKDVSCPIROVFGKQVPLIPDLNQTGKGFPSL 267
 DB 223 PSPRK- - - - - TPVADQRRR-SCKTAPASSKSYOTE-VPKRGKRSKMLPSK 267
 QY 268 AVSNEFEPSNHWKYSYLLFRVTRPGRREFNGMNGTNNENIDVNEELPARRKNRD 327
 DB 268 RVISRSQHDIIQMTCS- - - - - KRSGASEALIV- - - - - 297
 QY 328 GEKTFVAQMTVPDKNRRLQILDGEYEVAMQEMECPISKRATWETILDGKLPPEETS 387
 DB 298 -AKSMADVYKLGAKQVQTVIKHGPPRSNMKQRRRATPKK- - - - - PVGEVHS 344
 QY 388 QGFTLOFTLRWGETNDKSTAPIAKPLATRNSESLHOENKPGSVKPTQTITAVESLTTDL 447
 DB 345 - - - - - QFS- - - - - TGHANSPTIIIGK- - - - - AHTEKXVVPARP- - - - - 373
 QY 448 QTRKEKDTNENRQKRLRYQPLVNNTRQOTEARDL- - - - - HCPWCTLNCR 495
 DB 374 - - - - - YRLANFISQKMDFKEDLSGIAEMFTPVYKQBPQLSTC- 413
 QY 496 KLYSLKHLKLCCHSRPIFNYYVH--PKGARIDVINECYDGSYAGNPQDIHRQPGFAFSR 553
 DB 414 - - - - - HIAISSEMLLKQFGTDSGEBPLLPESSEFGANVFSAQNAQAQPSDKCSA 466
 QY 554 NGPVKRTPIYH--ILVCRPKRTKASMEFLSEDEGEVEQORTYSSGHNRLYRHSDTCLPL 611
 DB 467 SPPLRQCIRENGVNAKTPRNTYKMTSLTETKSTDETEPSKTYVSTAN- - - - - RSGRSTEB 521
 QY 612 RP-QEMEVDSDEKDEPMLEKTIIOIEFSDVNEGEKVMKMLHVMKHGFIANDQNM 670
 DB 522 RNIQKLPVESKS- - - - - EETNEIVE-CLIKRQAKTL- - - - - LQORREGEWKIEER 568
 QY 671 HACMLFVENYGOIK- - - - - IKKMLCRNFMHLVSMHDPNLSIMSIDKATYKLRMOQKLEGE 729
 DB 569 - - - - - FETTKENIEKEN- - - - - DE- - - - - IKKAMRSRTWQ 596
 QY 730 SASPANE- - - - - ETEBQNGTANGFSEINSKEKALETDSVSG 766
 DB 597 KCAPMSDLTDLKSLPTELMKDTARQONLQTDHAKAPKSEKX 640
 RESULT 11
 US-11-124-367A-434
 ; Sequence 434, Application US/11124367A


```
/ Publication No. US20060024700A1
/ GENERAL INFORMATION:
/ APPLICANT: Michele Cargill
/ APPLICANT: Hongjin Huang
/ TITLE OF INVENTION: Genetic Polymorphisms Associated with
/ FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
/ FILE REFERENCE: CLO01519.ORD
/ CURRENT FILING DATE: 2005-05-09
/ PRIOR FILING DATE: 2004-08-09
/ PRIOR APPLICATION NUMBER: US 60/568,846
/ PRIOR FILING DATE: 2004-05-07
/ PRIOR APPLICATION NUMBER: US 60/582,609
/ PRIOR FILING DATE: 2004-06-25
/ PRIOR APPLICATION NUMBER: US 60/599,554
/ PRIOR FILING DATE: 2004-08-09
/ NUMBER OF SEQ ID NOS: 34460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 434
/ LENGTH: 2896
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-124-367A-434

Query Match          3.4%; Score 138.5; DB 7; Length 2896;
Best Local Similarity 18.1%; Pred. No. 0.14;
Matches 149; Conservative 113; Mismatches 285; Indels 277; Gaps 35;

QY 12 NTCRG--GCGLHPTLADLIEH-----IEDNIDDPRLVLEQLQOPLVLA 58
DB 25 STCLFGRGIECDIRIOLPVVSKOKHIEHQBALHNSSTNPVNGSVLDEPVLKH 84
QY 59 SYINFMTDARBEOSLK-----KIQPKLSLTSSSVSGNVSTPPRH----- 104
DB 85 GGVITIDRSFYEHESLOSGRKSTFPFKIREQ--EPARVSSSSSDSDSDSGIDL 141
QY 105 -----SGSLTPV-----TPPTPSSSFSSSTPEPTQIYRFLRNLRIADIFLHRTLT 153
DB 142 KRRRVFSGHLRPELFDENLPNTPLK--RGEAPL----- 174
QY 154 YMSHNSRNINIKRT--FVYDMLSKVEKMK--GEOSHSLSAHLQUTFGFHRKNDK 207
DB 175 -----RRKSLVMTTPVLKIKIEQOPSGKSGS--EIHVEVKAOSLVISPPA 222
QY 208 PSPNSENEQNSVLEVLVVKVCHKKRQDVSCPIRQVPTGKQVPLIPDLNQTGKPNPPL 267
DB 223 PSBRK-----TPVADQRR--SCKTAASSKQTE--VPRKGGKSGNLRSK 267
QY 268 AVSSNEPEPSSHWKYSYSLFRVTRPGRRFNGMINGETNENIDVNEELPARRRKRED 327
DB 268 RVSISRQHDILQICS-----KRRSGASEANLIV----- 297
QY 328 GEKTVAQMTVDKRRRLDLDGEYVAMQEMEBECPISKRAWTETILDKRLPPETFS 387
DB 298 -AKSMADVVKGAQKOTQTVKIHGQPSRNNKQRRPAPYK-----PVGEVHS 344
QY 388 QGPTLOFTLRMTGEFNDSSTAPIAKPLATRNSESLHOENKPGSVKPTOTIAVKESLTDL 447
DB 345 -----QFS-----TGHANSPTIIIGK--AHTEKHVNPAP----- 373
QY 448 QTRKEKOTPNENRQKIRIFYOFLYNNNTROQTEARDL-----HCPWCTLNCR 495
DB 374 -----YRVANFISNQKMDFKEDLSGLAEMFKTPVKEQPOLSTSC- 413
QY 496 KLYSLKHLKLCHEFRINRYVH--PKGARIDVSNCECDGSAYNPODIHROPGFAPSR 553
DB 414 -----HIALSNSNLLGKQOGTDSGEBPLLPTESEFGVFPQAQVAAKQPSDKCSA 466
QY 554 NGPVKRTPLTH--ILVCRPKRTKASMESELESDGEVEOQRTYSSGHNRLVHSTCLPL 611
DB 467 SPPLARQCIKRENGVAKTPRNTYKMTSLKTSIDTETBSKVSTAN-----RSGRSTEF 521
QY 612 RP-QEMEVDSDEKQPEMLREKTIQIEFSDVNGEKEVNMKLVHVKHGFADINQMN 670
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DB 522 RNIOKLPVESKS-----EETNTEIVE--CIUKGQKATL-----LQRRREGMEKIERP 568
QY 671 HACTLFEVNYGQKI--IKKRLCNPMHLVSMEDPNLISIMSDKAVTKLRBQOQLEKES 729
DB 569 -----FETTKENIEIKEN-----DE--KKAKRRSRWQ 596
QY 730 SASPANE-----ETTEEONGTANGFSEINSKEKALETDSVSG 766
DB 597 KCAPMSDLTDLSLDTIELMKOTARGONILQTDHAKAPKSKG 640

RESULT 12
US-10-995-561-773
/ Sequence 773, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: Cargill, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CLO01559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ NUMBER OF FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 773
/ LENGTH: 3803
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-773

Query Match          3.3%; Score 135; DB 6; Length 3803;
Best Local Similarity 17.6%; Pred. No. 0.38;
Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;

QY 30 IEHIEDNIDDPRLVLEKQ----- 49
DB 1955 VEKLSIDTVASDPVGLQOLATTKQLOEELAEHOUVPEKLOKVADIMEIEGPARDH 2014
QY 50 LQOQTVYALSYINFMTDARRE-----QSLKKKTOP-----KLSL 86
DB 2015 VOETDSILSHSOSLSYLSARSSILQRAIOSQSGVSLSLQISGEVEQNLGKQVS 2074
QY 87 TLSSSVSGNVSTPPRHSSGSLTPVTPPIPPSSSFSSSTPEPTQ--IYRFLRNLRI 144
DB 2075 SLSSGVIOEALATNMK-----LKODIARQKSSLEATREMTVTRMETADSTT 2120
QY 145 PIFLHRTLTYSHNSRNINIKRTKFPVDMLSKV-----EKMKG-----EOSHSHS 191
DB 2121 AAVLOGKLAEVSQREQLCLOQ--EKESLSKLLPQAMFEBHLSGKIQQFWEKSRMLA 2178
QY 192 AHLQ--LTFGPFHKKRDPSPNSEQNSV--TLEVL----- 224
DB 2179 SGNOPODDOITTFPOIQIOLANEMEDQENLDTLEHLVETLSSCGPALDLQHQDRVQNL 2238
QY 225 -----LVVCHKKRQDVSCPIRQVPTGKQVPLIPDLNQTGKPNP--SLAVSSNEPEPS 277
DB 2239 KQFTELQTVKEREKQDASSCOEQLDEFKLVTRTQKMLKETEGSLPPTETSNAAELKQ 2298
QY 278 NSHWKYS-----SLFVTRPGRRFNGMINGETNENI----- 311
DB 2239 IEHL-KSLDDWASKGTIVEINCKGTSLEMLMEITAPDQOGKGTSLPVGSSVGSVN 2357
QY 312 -----DVNEELPARRRKREDGEKTVAQMTVPDKRRLLQDLS-----EYEVAMOE 358
DB 2358 GYHTCKDLTE-----IQCDMSDVNLYKFKLGGVLIHEROBESIQAILNR 2399
QY 359 MEBOPISKKRAWTETILDKR--LPPEFSGOPLQFTLAWGTGNTDKSTAPIAKPLAT 416
DB 2400 MEE--VHKANSVUQWLESKEEVLKSMAMS--SPKTIETVAQAQESNAFLAEL----- 2450
QY 417 RNSESLQENKPGSVKPTQTIAYVESLTTDQTRKEKQTPN-----ENRQKIRIFYOFLYN 472
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Db 2451 -----EQNSPKIOK-----VKEALAGLVT-----YPSQEAENWKKIOEELNSRWE 2492
Qy 473 NNT-----ROOTEARDLHC-----PWC-----TLNCRKLY 498
Db 2493 RATEVTVARQROLESASHLACFOAAESQLRPWLMEKELMMGYLGPLSIDPNNMLNOK-- 2550
Qy 499 SLKHLKLCGSRPFTFNVVYHPKCARIDVSINECYDGSYAGNPQDIIHQRFAPFSRNGPYK 558
Db 2551 ---QOVQFMKEFEARQOHEQ-----LNEAAQGIITG-----PDVSLSTSQVQ 2592
Qy 559 RTPITHLVCRPRTKYSAMEFLESEDEGEVOQRTYSSGHNRLYFHSDTCLPLRPOEMEV 618
Db 2593 KE-----LQSIHQKWELTDKLNSSSQIDQAIKVSQYOELLQDISEKVRAYVGRSLV 2646
Qy 619 DSEDEKDEPWLREKTIITQIEEFSVDNVEGEKVKMLNLMYMGKGFADNQMNAICMLFVE 678
Db 2647 QSAISTOPEAVKO-----QLEETSEIRSDLEQD-----HEVKE---AQTLCDLSVLIGE 2694
Qy 679 NYGOKIIRKNCNFMHLVSMHDFNLISMSIDKAVTKLEMOQ----- 723
Db 2695 QYKDELKRL-ETVALPLQGLDLADRLNRLQALASTQOQOQMFDELRTWLDKQSQ 2753
Qy 724 -----KLEGESASPANEITEBQNGTANGFSEINSKEKALETDSVSVSKSQKQ 774
Db 2754 QAKNCPISAKLERLOQOLQENEFQKSLNQHSGSYEVITVAEGBSLLSVPPGEEKRTLQV 2813
Qy 775 KL 776
Db 2814 QL 2815

RESULT 13

US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-771

Query Match 3.3%; Score 135; DB 6; Length 3960;
Best Local Similarity 17.6%; Pred. No. 0.4;
Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;
Qy 30 IEHEDHIDTPDPRVLEKQ-----E 49
Db 1955 VEKLSITVASDPGVLOEQALATTQOLQBELAHQVPEYKQKVARDMIEBGEAPDRHR 2014
Qy 50 LQOPTVALSYINRFMTDAARR-----QESLKCKIOP-----KLSL 86
Db 2015 VOERTDLSLHPQSLSYSLAERSLLQKALAQOSQVQESLESLLQSGIVEQNLEGKQVS 2074
Qy 87 TLSSSVRGAVSPRPRISSGSLTPPVPTPTSSSPSSPTPTETO--IYRFLRTRLIA 144
Db 2075 SLSSGVIQKALATNMK-----LKODIAKQKSLKXTRREMYTRFEMTAOSTT 2120
Qy 145 PIFLHRTLYTMSHRNSRNTIKRKTFFKVDMLSKV-----EKWKG-----EOSHSLIS 191
Db 2121 AAVTQGLAIVSQRFEOQLCLOQ--EKSSILKLLPLQAEHFEHLISGLQOFMEKSKMLA 2178
Qy 192 AHLQ--LTFTGFHAKNDKPSNSENQNSV-TLEVL----- 224

Db 2179 SGNPQDQITHFQOIQEILNLEMEQOENIDLTLEHLVTELSGCGFALDLCOHQDRVQNLR 2238
Qy 225 -----LVKXCHKKRDVSCPIROVPTGKQVPLIPDLNQTGKNFP--SLAVSSNEFES 277
Db 2239 KQFTELQTKERKEDASSQOQDLEFRKLVTRPQKMLKETBSQSIDPPTTSNAKLEKQ 2298
Qy 278 NSHMVKS-----SLFRVTRGRREBNMGINGETNENT---- 311
Db 2299 IEHL-KSLDDMAKSKTLVEINCKGTSLENILMETAPDSQOKGTSILPSVSSVSGSVN 2257
Qy 312 -----DVNEELPARKNRNDEGEKTFVAQMTVFDRKRLQLLDG-----EYVAMQE 358
Db 2358 GYHTCKDLE-----IQCMSDVNLKYEKLGVLHERQESLOAIILR 2399
Qy 359 MECPISKRAWTETILDKR--LPPFETPSQPTLOFLRMTGETNDSAPIAPLAT 416
Db 2400 MEE--VHKANSYTLQWLESKEBYLSMDMS--SPITTEYVKAQAEKNKAFLEL----- 2450
Qy 417 RNSSELIHQENKQSVKPTQTIIVKESLTTDLQTRKEKQTPN---ENRQKLRIFYQFLYN 472
Db 2451 -----EQNSPKIOK-----VKEALAGLVT-----YPSQEAENWKKIOEELNSRWE 2492
Qy 473 NNT-----ROOTEARDLHC-----PWC-----TLNCRKLY 498
Db 2493 RATEVTVARQROLESASHLACFOAAESQLRPWLMEKELMMGYLGPLSIDPNNMLNOK-- 2550
Qy 499 SLKHLKLCGSRPFTFNVVYHPKCARIDVSINECYDGSYAGNPQDIIHQRFAPFSRNGPYK 558
Db 2551 ---QOVQFMKEFEARQOHEQ-----LNEAAQGIITG-----PDVSLSTSQVQ 2592
Qy 559 RTPITHLVCRPRTKYSAMEFLESEDEGEVOQRTYSSGHNRLYFHSDTCLPLRPOEMEV 618
Db 2593 KE-----LQSIHQKWELTDKLNSSSQIDQAIKVSQYOELLQDISEKVRAYVGRSLV 2646
Qy 619 DSEDEKDEPWLREKTIITQIEEFSVDNVEGEKVKMLNLMYMGKGFADNQMNAICMLFVE 678
Db 2647 QSAISTOPEAVKO-----QLEETSEIRSDLEQD-----HEVKE---AQTLCDLSVLIGE 2694
Qy 679 NYGOKIIRKNCNFMHLVSMHDFNLISMSIDKAVTKLEMOQ----- 723
Db 2695 QYKDELKRL-ETVALPLQGLDLADRLNRLQALASTQOQOQMFDELRTWLDKQSQ 2753
Qy 724 -----KLEGESASPANEITEBQNGTANGFSEINSKEKALETDSVSVSKSQKQ 774
Db 2754 QAKNCPISAKLERLOQOLQENEFQKSLNQHSGSYEVITVAEGBSLLSVPPGEEKRTLQV 2813
Qy 775 KL 776
Db 2814 QL 2815

RESULT 14

US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

Query Match 3.3%; Score 135; DB 6; Length 5335;
Best Local Similarity 17.6%; Pred. No. 0.61;

Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;

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QY 30 IEHEDNHITDTPRVLKQ-----E 49
DB 1863 VEKLSDTVASDPGVLOQLATTQLOEELAEHQVVEKLOKVARDIMEIEGEPADHRH 1922
QY 50 LQOPTVALSYINRMTJAAARE-----QESLKKKTOP-----KLSL 86
DB 1923 VQETTSILSHQOSLSYSLAEBSLLOKALMOSQSVQESLSLQSIGEVONLEBKQVS 1982
QY 87 TLSSSVSGKNSVTPPHSSGSLTPVTPPTPSSFRSTPPEPQ--YRPLRTNLLA 144
DB 1983 SLSSGVLOEALATNMK-----LKODIAROKSSLEATREMTTFRMETADSTT 2028
QY 145 PIFLIRTLTYMSHRNRTNIRKRTFKVDMLSKV-----EKMKG-----EOSHSL 191
DB 2029 AAVLGKLAESQREQLCLOOQ--EKESLKKLLPQAMFELHSGKLOQFMENKSRMLA 2086
QY 192 AHLQ--LFTGPFHKNKDPSPNSENQSV--TLEVL----- 224
DB 2087 SGNQPDODITTFHQIOELNLEMEQOENLDTLEHLVTELSGCFALDCQHODRVQNL 2146
QY 225 ----LVKVCCHKRQDVCPTRQVPTGKKQVPLIDLMOTKGNFP--SLAVSNPEPS 277
DB 2147 KQFTLEQKTVKEREKQDASSCOEQLDEFKLVTPFKMLKETGSIPTETSSAKLEKQ 2206
QY 278 NSHMVKS-----SILFRTPRGRREFNGMNGETNENI----- 311
DB 2207 IEHL-KSLDDWASKGLVEEINCKGTSLENLIMETAPDSQKTSILPSVSGSVGN 2265
QY 312 ----DVNEELPARKRREDEGEKTFVAQMTVPDKNRRLQLLDG-----EYEVAMOE 358
DB 2266 GYHTCKDLTE-----IQCDMSDVNLKYEKLGVLHERQESLQALINR 2307
QY 359 MECPISKRRATWETILDKR--LPPETFSOGPTLOFTLMTGETNDKSTAPLAPLAT 416
DB 2308 MEE--VHKANSVLOMLESKKEVLKSMQDMS--SPKTETTVAKQAESNAKFLAEL----- 2358
QY 417 RNSESLHQENKPGSVKPTOTIAVESLTTDLQTRREKQTPN---ENRQKLAIFYOFLYN 472
DB 2359 ----EONSPIKIQ-----VKELAGLLVT-----YPSQEAENMKKIOEBINSRWE 2400
QY 473 NNT-----ROOTEARDDLHC-----PMC-----TLNCRKLY 498
DB 2401 RATEVTVARORQLESASHLACFOAAESQLRPMLMEKELMVGPLSIDPMMLAOK-- 2458
QY 499 SLKHLKLCHSRPFIFNYVYHPKGARIDVINSCEYDGSVAGNPDIIHQGFASFNGPYK 558
DB 2459 ----QOVQFMLKEFEARRQOHEQ-----LNEAAGIILTG-----PGDVSLSSTQVQ 2500
QY 559 RTPITHILVCRPKTKASMEFLESDEGEVBOQRTYSSGHNRLYTHSDCLPLRQEMEV 618
DB 2501 KE-----LOSINQKMWELTDKLNRSQIDQAIKSTYOYELLDLSEKVAVQORLSV 2554
QY 619 DSEDEKDEPMLEKETTITQIEEFSDVNBEKEVAKMLNLMVHGCFIADQNMHACLFVE 678
DB 2555 QSAISTQEPRAVQO-----QLEETSEIRSDLEQJD-----HEVGE--AQLCDBELSVLGE 2602
QY 679 NYGQKIIKKNCGRNFMHLVSMHEDPNLISIMSIDAVTKLRMOQ----- 723
DB 2603 QYKQELKKRL--ETVALPLOGLEDLAADRINRLALASTQOFOQMFDELFRTMLDKOSO 2661
QY 724 ----KLEKGSASPANEITEBQNGTANGSEINSKKALETDSVGSVQSKQ 774
DB 2662 QAKNCPISAKLERLOSQLOEENEFQSLNQHSGSYEVIVABGESLILSVPEEKRTLON 2721
QY 775 KL 776
DB 2722 QL 2723

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Sequence 779, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 779
LENGTH: 5415
TYPE: prt
ORGANISM: Homo sapiens
US-10-995-561-779

Query Match 3.3%; Score 135; DB 6; Length 5415;
Best Local Similarity 17.6%; Pred. No. 0.62;
Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;

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QY 30 IEHEDNHITDTPRVLKQ-----E 49
DB 1955 VEKLSDTVASDPGVLOQLATTQLOEELAEHQVVEKLOKVARDIMEIEGEPADHRH 2014
QY 50 LQOPTVALSYINRMTJAAARE-----QESLKKKTOP-----KLSL 86
DB 2015 VQETTSILSHQOSLSYSLAEBSLLOKALMOSQSVQESLSLQSIGEVONLEBKQVS 2074
QY 87 TLSSSVSGKNSVTPPHSSGSLTPVTPPTPSSFRSTPPEPQ--YRPLRTNLLA 144
DB 2075 SLSSGVLOEALATNMK-----LKODIAROKSSLEATREMTTFRMETADSTT 2120
QY 145 PIFLIRTLTYMSHRNRTNIRKRTFKVDMLSKV-----EKMKG-----EOSHSL 191
DB 2121 AAVLGKLAESQREQLCLOOQ--EKESLKKLLPQAMFELHSGKLOQFMENKSRMLA 2178
QY 192 AHLQ--LFTGPFHKNKDPSPNSENQSV--TLEVL----- 224
DB 2179 SGNQPDODITTFHQIOELNLEMEQOENLDTLEHLVTELSGCFALDCQHODRVQNL 2238
QY 225 ----LVKVCCHKRQDVCPTRQVPTGKKQVPLIDLMOTKGNFP--SLAVSNPEPS 277
DB 2239 KQFTLEQKTVKEREKQDASSCOEQLDEFKLVTPFKMLKETGSIPTETSSAKLEKQ 2298
QY 278 NSHMVKS-----SILFRTPRGRREFNGMNGETNENI----- 311
DB 2299 IEHL-KSLDDWASKGLVEEINCKGTSLENLIMETAPDSQKTSILPSVSGSVGN 2357
QY 312 ----DVNEELPARKRREDEGEKTFVAQMTVPDKNRRLQLLDG-----EYEVAMOE 358
DB 2358 GYHTCKDLTE-----IQCDMSDVNLKYEKLGVLHERQESLQALINR 2399
QY 359 MECPISKRRATWETILDKR--LPPETFSOGPTLOFTLMTGETNDKSTAPLAPLAT 416
DB 2400 MEE--VHKANSVLOMLESKKEVLKSMQDMS--SPKTETTVAKQAESNAKFLAEL----- 2450
QY 417 RNSESLHQENKPGSVKPTOTIAVESLTTDLQTRREKQTPN---ENRQKLAIFYOFLYN 472
DB 2451 ----EONSPIKIQ-----VKELAGLLVT-----YPSQEAENMKKIOEBINSRWE 2492
QY 473 NNT-----ROOTEARDDLHC-----PMC-----TLNCRKLY 498
DB 2493 RATEVTVARORQLESASHLACFOAAESQLRPMLMEKELMVGPLSIDPMMLAOK-- 2550
QY 499 SLKHLKLCHSRPFIFNYVYHPKGARIDVINSCEYDGSVAGNPDIIHQGFASFNGPYK 558
DB 2551 ----QOVQFMLKEFEARRQOHEQ-----LNEAAGIILTG-----PGDVSLSSTQVQ 2592
QY 559 RTPITHILVCRPKTKASMEFLESDEGEVBOQRTYSSGHNRLYTHSDCLPLRQEMEV 618
DB 2593 KE-----LOSINQKMWELTDKLNRSQIDQAIKSTYOYELLDLSEKVAVQORLSV 2646

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QY 619 DSEDEKOPWLEKRTTTOIEBESDVNGEKEVWKMLNHLVWKHGFADNOMHACMLFVE 678
DB 2647 OSAISTOPFAVKQ---OLEETSEIRSDLEOLD---HEVKE---AQTLCDLAVLIGE 2694
QY 679 NYGOKIHKKNLGRNFMHLVSMHDFNLISIMSIDKAVTKLREMOQ----- 723
DB 2695 OYIKDELKKRL-ETVALPLOGLEDLADRINRLQALASTQOFQOMFDELRTWDDKQSQ 2753
QY 724 -----KLEKSESASPANEEITEBQNGTANGFSEINSKEKALETDSVSVSKQSKQ 774
DB 2754 QAKNCPIASAKLERLQSQLOENEEFOKSIHQSGSYEVYVAEGESLILSVPPGEKERTLOV 2813
QY 775 KL 776
DB 2814 QL 2815

Search completed: April 7, 2006, 13:21:45
Job time : 33 secs